



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96696

TO: Medina A Ibrahim
Location: CM1/9E03/9E12
Art Unit: 1638
Monday, June 23, 2003

Case Serial Number: 010731

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Ibrahim,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 04:26:33 ; Search time 1133 Seconds

(without alignments)
6421.625 Million cell updates/sec

Title: US-10-010-731-13

Perfect score: 250
Sequence: 1 GGGGATCCCAATCAATCA.....AAAAGATGTAAGATCCCC 250

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	234	93.6	406	8	AF319468	AF319468 Medicago
2	156.4	62.6	468	8	PEADRR230A	L01578 Pea (p1230)
3	156.4	62.6	468	8	PSPT230	X52225 P.sativum p
4	154.8	61.9	363	8	AF139018	AF139018 Pisum sat
5	119.4	47.8	494	6	AX252303	AX252303 Sequence
6	113	45.2	496	8	AB020613	AB020613 Vigna rad
7	109.8	43.9	459	8	VUSTORED	X16877 Vigna ungu
8	98	39.2	456	8	PEADRR230B	L01579 Pisum sativ
9	98	39.2	456	8	PSPT19	X52224 P.sativum p
10	49.2	19.7	380	8	AB049718	AB049718 Pisum sat
11	41.8	16.7	922	8	MTN1GENE	Y10456 Medicago tr
12	40	16.0	141	6	A27063	A27063 L.ciceria AF
13	40	16.0	141	6	A39547	A39547 Sequence 35
14	40	16.0	141	6	AR050147	AR050147 Sequence
15	40	16.0	141	6	AR130266	AR130266 Sequence
16	40	16.0	141	6	I23722	I23722 Sequence 35
17	38.2	15.3	200218	2	AC123956	AC123956 Mus muscu
18	38.2	15.3	206082	2	AC126936	AC126936 Mus muscu
19	38	15.2	281	8	AF293407	AF293407 Phaseolus
20	37.8	15.1	170559	2	AC026989	AC026989 Homo sapi
21	37.8	15.1	182997	9	AL355332	AL355332 Human DNA
22	37.6	15.0	133418	9	AL353709	AL353709 Human DNA
23	37.6	15.0	157812	2	AC055805	AC055805 Homo sapi
24	37.4	15.0	68912	9	AC097490	AC097490 Homo sapi
25	37.4	15.0	138868	2	AC079302	AC079302 Homo sapi
26	37.2	14.9	134286	9	AC025771	AC025771 Homo sapi
27	37.2	14.9	170272	9	AC024589	AC024589 Homo sapi
28	36	14.4	170670	2	AC121758	AC121758 Homo sapi
29	36	14.4	171998	9	AC026120	AC026120 Homo sapi
30	36	14.4	198695	10	AC090648	AC090648 Genomic s
31	36	14.4	212722	2	AC087158	AC087158 Mus muscu
32	36	14.4	223412	2	AC124722	AC124722 Mus muscu
33	35.6	14.2	130754	2	AC093325	AC093325 Homo sapi
34	35.6	14.2	152779	2	AC015837	AC015837 Homo sapi
35	35.6	14.2	207259	2	AC110899	AC110899 Mus muscu
36	35.4	14.2	94739	9	AP001964	AP001964 Homo sapi
37	35.4	14.2	169091	2	AC025852	AC025852 Homo sapi
38	35.4	14.2	187372	2	AC122453	AC122453 Mus muscu
39	35.4	14.2	220470	2	AC122327	AC122327 Mus muscu
40	35.4	14.2	226366	2	AC126045	AC126045 Mus muscu
41	35.2	14.1	434	8	GMSE60	Z13956 G.max mRNA
42	35.2	14.1	9386	1	AE000791	AE000791 Borrelia
43	35.2	14.1	205409	2	AC121939	AC121939 Mus muscu
44	35	14.0	46831	2	AC087204	AC087204 Homo sapi
45	35	14.0	107037	2	AF186029	AF186029 Homo sapi

ALIGNMENTS

RESULT 1
AF319468
LOCUS AF319468 406 bp mRNA linear PLN 14-DEC-2000
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.
ACCESSION AF319468
VERSION AF319468.1 GI:11762085
KEYWORDS
SOURCE Medicago sativa.
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 406)
REFERENCE
1 Liang, J., Shah, D.M., Wu, Y.S., Rosenberger, C.A. and Hakim, S.
AUTHORS

TITLE	JOURNAL	MOL. PLANT MICROBE INTERACT.	4 (4), 324-331 (1991)
FEATURES	COMMENT	On Feb 8, 2002 this sequence version replaced gi:247416.	
gene	1799696		
CDS			
gene			
1..468			
/dev_stage="immature"			
/db_xref="taxon:3888"			
/tissue_type="pod tissue treated with Fusarium solani conidia"			
/dev_stage="immature"			
1..468			
/gene="DRR230-a"			
78..296			
/gene="DRR230-a"			
/function="unknown"			
/standard_name="pathogenesis related protein"			
/note="p1230"			
/codon_start=1			
/evidence=experimental			
/product="disease resistance response protein"			
/protein_id="AA079117.1"			
/db_xref="GI:169074"			
/translation="MEKSLACLISFLILVLFVAOEIVSEANTCENLAGSYKGVCGFC			
CDRHCRTQEGALISCRCDRDFRCMCTKNC"			
159..293			
/gene="DRR230-a"			
/product="disease resistance response protein"			
/function="unknown"			
/note="determined by in vitro cleavage with microsomal membranes"			
/evidence=experimental			
BASE COUNT	153 a	88 c	84 g
ORIGIN			
Query Match	62.6%;	Score 156.4;	DB 8; Length 468;
Best Local Similarity	80.0%;	Pred. No. 5e-34;	
Matches 184;	Conservative 0;	Mismatches 46;	Indels 0;
Gaps 0;			
13 CTAATCAAACACTVMTSGAGAGAATACACTAGCTGCTTATGCTTCCTCTTGGTCTCT	72		
11 11			
67 CTTAAGAAGCATGAGAGAAGAAATACACTAGCTTGTCTCTCTCTCTCTCTCTCTCTCT	126		
73 TTGTTGCACAGAATTTGTTGTTGACAGACGACAGACACTGTGAGATTTGGCAGATAAT	132		
11 11			
127 TTGTTGCACAGAATTTGTTGTTGACAGACGACAGACACTGTGAGATTTGGCAGATAAT	186		
133 ATAGGAGGACCTGCTTGTAGTGTGTTGACACTACTGACACCAACCAAGAGACGAGTTA	192		
11 11			
187 ATAGGAGGAGTATGCTTGTGTTGACAGTGTGACCTGACATGAGAACACAGAGGCGCAATTA	246		
193 GTGGAAGGTGAGGAGCACTTCGCTGCTGCTGTACTATAAAGATGTTAA	242		
11 11			
247 GCGGACAGATGACGAGGATGACTTTCGCTGTGTTGTCACATAAAACGTGTTAA	296		
RESULT 3			
PPSP1230			
LOCUS			
DEFINITION	PPSP1230		
ACCESSION	X52225		
VERSION	X52225.1		
KEYWORDS	GI:22208748		
SOURCE	secreted protein.		
ORGANISM	pea.		
	Pisum sativum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;		
	Pisum.		
REFERENCE			
1			

FEATURES	LOCATION/Qualifiers	1..363	61.9%	Score 154.8	DB: 8	Length 363
gene	/organism="Pisum sativum"					
	/cultivar="GreenFeast"					
	/db_xref="taxon:3888"					
	1..363					
	/gene="DRR230"					
	56..274					
	/gene="DRR230"					
	/note="Ozone-induced, similar to the Pisum sativum cv. Alaska product encoded by GenBank Accession Number L01578"					
	/codon_start=1					
	/product="disease resistance response protein 230 precursor"					
	/protein_id="PAG33285.1"					
	/db_xref="GI:12002299"					
	/translation="MKRSLLACSLFLLVLFIAEIVSEANTCENLAGSIKYGVCFGC					
	CDRRCRQBEAISGCRDPRFCWCTKNC"					
BASE COUNT	113 a	68 c	74 g	108 t		
ORIGIN						
Query Match		61.9%	Score 154.8	DB: 8	Length 363	
Best Local Similarity	79.6%	Pred. No. 1.5e-33				
Matches 183	Conservative 0	Mismatches 47	Indels 0	Gaps 0		
QY	13 CTAAATCAACATGATGAGAGAGAAATCACTAGCTGCTATGCTTCCTCTTGGTCTCT	72				
Db	45 CTTAAGAAGCCATGAGAGAAATCACTAGCTGCTTCCTCTCTCTCTCTCTCTCTCT	104				
QY	73 TTGTTGCACAGAATTTGTGGTGCACAGGCCACATGTGACAAATTTGGCACATAAT	132				
Db	105 TTATTGACACAGAATAGTGGTGAAGCAACACATGTGAAATTTGGCTGTTAT	164				
QY	133 ATAGGGACACCTGTTAGTGTGTGACACTGCACACCAACCAAGAGAACGACGTA	192				
Db	165 ATAGGAGATGCTGTTGGTGGATGTGACGCTCACTGTAGAACACAAAGCGGCATTA	224				
QY	193 GTGGAAGGTGAGGACGACTCCGCTGCTGCTACTAAATGTTAA	242				
Db	225 GCGGACAGATGAGGAGATGACTTTCGCTGTTGTCACCTAAAAACTGTAA	274				
RESULT 5						
AX252303						
LOCUS	AX252303	494 bp	DNA	linear	PAT 05-OCT-2001	
DEFINITION	Sequence 5 from Patent WO0168887.					
ACCESSION	AX252303					
VERSION	AX252303.1	GI:15985643				
KEYWORDS						
SOURCE	soybean.					
ORGANISM	Glycine max					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Hypallergenic transgenic soybeans					
	Patent: WO 0168887-A 5 20-SEP-2001;					
	E. I. du Pont de Nemours and Company (US);					
	INTERNATIONAL, INC. (US)					
REFERENCE						
AUTHORS	Jung, R. and Kinney, A. J.					
TITLE	Hypallergenic transgenic soybeans					
JOURNAL	Patent: WO 0168887-A 5 20-SEP-2001;					
	E. I. du Pont de Nemours and Company (US);					
	INTERNATIONAL, INC. (US)					
FEATURES						
source	Location/Qualifiers					
	1..494					
	/organism="Glycine max"					
	/db_xref="taxon:3847"					
BASE COUNT	153 a	97 c	103 g	134 t	7 others	
ORIGIN						

Query Match	47.8%	Score 119.4	DB 6	Length 494
Best Local Similarity	74.9%	Pred. No. 1.8e-23		
Matches 179	Conservative 0	Mismatches 51	Indels 9	Gaps 2
OY	13	CTAATCAACATATGAGAGAAATCACTACCTAGCTGCTTATGCTTCCTCTTCTGGTTCCT	72	
Db	35	CTAATTAAGCCATGAGAGAAATCAATAGCTGGTGTGCTTCCTCTTCCTTGCCTCT	94	
OY	73	TTGTGACCAAGAAATTTGTGGT---ACAGAAAGCAAGACATGTGAGAAATTTGGCAGATA	129	
Db	95	TTGTGCTCAAGAAATTTGTGGTCCAAACTGAGGCAAGACATTGGCAGAACCTGGGTGATA	154	
OY	130	AATATAGGGGACCATGCTT-----TAGTGGTTTGACACTCACTGCACAAACAAAGAGA	183	
Db	155	CATACAGGGGCTCATGCTTCACCACTGCACGCTCGATGATCACTGCACAAAGCAAGAGAC	214	
OY	184	ACGCAAGTTAGTGGAGGTGTGGGAGACGCTTCGCTGGTGTGTACTAAAGATGTTAA	242	
Db	215	ACTTGCTCAGACGAGATCAGGAGCGATTTTCCTGTGGTGTGACCAACAAACTGTGTA	273	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AB020613	Vigna radiata mRNA for PDI1, complete cds.	AB020613	AB020613.1	GI:18146787	PDI1.	Vigna radiata (strain:B20P5 9-3-2-2) immature seed cDNA to mRNA, clone_11b:B20 clone;pdf-1.
AB020613	Vigna radiata mRNA for PDI1, complete cds.	AB020613	AB020613.1	GI:18146787	PDI1.	Vigna radiata (strain:B20P5 9-3-2-2) immature seed cDNA to mRNA, clone_11b:B20 clone;pdf-1.

REFERENCE
1. Ishimoto, M. and Kaga, A.
TITLE
Mungbean defensin
JOURNAL
Published Only in Database (2002)
REFERENCE
2 (bases 1 to 496)
AUTHORS
Ishimoto, M. and Kaga, A.
TITLE
Direct Submission
JOURNAL
Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National
Agricultural Experiment Station, Laboratory of Plant Biotechnology,
6-12-1 Nishitokatsu, Fukuyama, Hiroshima 721-8514, Japan
(E-mail:ishimoto@cgc.affrc.go.jp, Tel:+81-849-234100(ex.231),
Fax:+81-849-247893)

FEATURES	
source	Location/Qualifiers
polyA_site	1..496
	/organism="Vigna radiata"
	/strain="B20F5_9-3-2-2"
	/db_xref="taxon:157791"
	/clone="pdf-1"
	/rissue_type="immature seed"
	/clone_1fb="B20"
	1..496
	/gene="pdf1"
	46..273
CDS	/gene="pdf1"
	/codon_start=1
	/product="PDF1"
	/protein_id="BA82453.1"
	/db_xref="GI:18146788"
	/translation="MEKKSLAGCLFLVLFVAQEVAVQTEAKTCENLANTYRSPCTFTGSCDDICKNKHILRSRCRDRFCWCTRC"
	496

BASE COUNT	148 a	104 c	106 g	138 t	
ORIGIN	/gene="pDf1" /note="17 a nucleotides"				
Query Match	45.28;	Score 113;	DB 8;	Length 496	
Best Local Similarity	73.12%;	Pred. No. 1,2e-21;			

Matches	1/5:	Conservative	0:	Mismatches	55:	Indels	9:	Gaps	2:
OY	13	CTAATCAACTATGAGAGAAGAAATCAGTACGTGCTTATGCTTCTCTTCTTGGTCTCT							72
Db	35	CTAATCAAGCCATGAGAGAAGAAATCAGTACGTGCGGGATTTGTGCTCTCTTCTTCTTCTCT							94
OY	73	TTGTATGCACAGAAGAAATTTGGTGT---							
Db	95	TTGTATGCCTCAAGAAAGTTATGTGTGCGACACTGAGGCCAAAGACTTTGGAGAACTCGCGGAATA							154
OY	130	AATATATGGGGACCATGCTT-----							
Db	155	CTTACAGGGGTCCATGTCTTACCAACACTGCGACACTGCGAATGATCAGTCAAGAAACAAAGAAC							214
OY	184	ACGCGATTATGAGAGAGGTGTATGGGACGACCTTCCCGTGTGGGTGTCTATAAAGATCTTAA							242
Db	215	ACTTGGAGGAGTGTGCGACGTGTCAGGACGCAATTTCCCGTGTGGTGTGCACTGTGAAGAACTGTTAA							273

RESULT 7	VSTORED	459 bp	mRNA	linear	PLN 12-SEP-1992
LOCUS	Vigna unguiculata	CDNA	for stored	cotyledon	mRNA.
DEFINITION	X16877				
ACCESSION	X16877.1	GI:22075			
VERSION					
KEYWORDS					
SOURCE	Vigna radiata				
ORGANISM	Vigna radiata				

REFERENCE	1 (bases 1 to 459)
AUTHORS	Yamauchi, D.
TITLE	Direct Submission
JOURNAL	Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo Metropolitan University, Fukuoka 2-1, Setagaya-ku, Tokyo 158, Japan
REFERENCE	2 (bases 1 to 459)
AUTHORS	Ishibashi, N., Yamauchi, D. and Minamikawa, T.
TITLE	Stored mRNA in cotyledons of <i>Vigna unguiculata</i> seeds: nucleotide sequence of cloned cDNA for a stored mRNA and induction of its synthesis by precocious germination
JOURNAL	PLANT MOL. BIOL. 15 (1), 59-64 (1990)
MEDLINE	91353865
PUBMED	2103443

FEATURES	source	Location/Qualifiers
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		/db_xref="taxon:157791"
		/clone="pSAS10"
		/issue_type="cotyledon"
		/clone_lib="lambda g110"
		/dev_stage="seed"
CDS		14..241
		/note="pSAS10 ORF"
		/codon_start=1
		/protein_id="CAA34760.1"
		/db_xref="GI:22076"
		/db_xref="SWISS-PROT:P18646"
		/translation="MEKKSITAGLGFLEVLVEVAQEVVQASAKTCENLVDTYRGPCF"
		"TGSCDDHCKNEHLISGCRDQVPCWCTRNC"
BASE COUNT		136 a 91 c 99 g 133 t
ORIGIN		

Query Match	43.9%	Score 109.8	DB 8	Length 459;
Best Local Similarity	72.4%	Pred. No. 1e-20;		
Matches 173:	Conservative	0;	Mismatches 57;	Indels 9;
			Gaps	2.
OY	13	CTAATCAACATGATGAGAGAATAACTAGCTGCTTATGCTTCTCTTCTGTTCTCT	72	
cb	3	CTAATTAAGCCATGTGAGAGAATAATCAATCGCTGGTATATGGTTCTCTCTTCTTCTCTCT	62	

[illegible]

Db	60	ACTAAGATTGAGAGAGAAATTCAC	TAGCTGCTTGTCTTCCTCCTCCTGTTCTC	119
QY	72	TTTGTGTGACAGAAATTTGTGTGTCAGAGAACCCAGAACATGTGAGAAATTTGGCAGATAAA	131	
Db	120	TTTGTGTGACAGAAATTTGTGTGTCAGAGAACCCAGAACATGTGAGAAATTTGGCAGATAAA	179	
QY	132	TATAGGGAGACCATGCTT-----TAGTGTGTTGTGACACTACCTGACACACCAAGAGAAC	185	
Db	180	TACAGGGAGATGATGCTTTCACGAATGCTAGCTGTATGTATGATCTACGCAAGAACCAAGAGCCGAC	239	
QY	186	GCAGTGTAGTGAAGGTGTAGGAGACACTCCGCTGCTGTGTACTATAAAGATGTTAAGA	245	
Db	240	TTAATCAGTGGACGCT--GCCATGACTGGAATATGTTTCTACTCTCAAAACTGTTAAGA	296	
RESULT 9				
PSP139				
LOCUS	PSP139	456 bp	mRNA	linear PLN 09-AUG-2002
DEFINITION	P.sativum p139 mRNA.			
ACCESSION	X52224			
VERSION	X52224.1 GI:22208744			
KEYWORDS	secreted protein.			
SOURCE	pea.			
ORGANISM	Pisum sativum			
REFERENCE	1			
AUTHORS	Chiang,C.C. and Hadwiger,L.A.			
TITLE	The fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins			
JOURNAL	Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)			
MEDLINE	92190628			
REFERENCE	2 (bases 1 to 456)			
AUTHORS	Chiang,C.			
TITLE	Direct Submission			
JOURNAL	Submitted (03-AUG-1990) Chiang C., Washington State University, Dept. of Plant Pathology, Pullman, WA 99164-6430, USA			
FEATURES	Location/Qualifiers			
source	1..456			
gene	/organism="Pisum sativum"			
	/db_xref="taxon:3088"			
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CDS	/gene="p139"			
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	/protein_id="CAA36473.1"			
	/db_xref="GI:22208745"			
	/translation="MEKSLAALFSLILLYFVAQELIVTEANTCEHLADYRVCCT NASCDHCKNKAHLISGCHMKPCFQNC"			
	69..152			
sig_peptide	/gene="p139"			
	153..290			
mat_peptide	/gene="p139"			
	/product="unamed"			
BASE COUNT	155 a 81 c 79 g 141 t			
ORIGIN				
Query Match	39.2%; Score 98; DB 8; Length 456;			
Best Local Similarity	72.1%; Pred. NO. 2.4e-17;			
Matches	173; Conservative 0; Mismatches 55; Indels 12; Gaps 3;			
QY	15	AATCAACTATGAGAGAGAAATTCAC	TAGCTGCTTGTCTTCCTCCTGTTCTC	71
Db	60	ACTAAGATTGAGAGAGAAATTCAC	TAGCTGCTTGTCTTCCTCCTGTTCTC	119
QY	72	TTTGTGTGACAGAAATTTGTGTGTCAGAGAACCCAGAACATGTGAGAAATTTGGCAGATAAA	131	
Db	120	TTTGTGTGACAGAAATTTGTGTGTCAGAGAACCCAGAACATGTGAGAAATTTGGCAGATAAA	179	
QY	132	TATAGGGAGACCATGCTT-----TAGTGTGTTGTGACACTACCTGACACACCAAGAGAAC	185	
Db	180	TACAGGGAGATGATGCTTTCACGAATGCTAGCTGTATGTATGATCTACGCAAGAACCAAGAGCCGAC	239	
QY	186	GCAGTGTAGTGAAGGTGTAGGAGACACTCCGCTGCTGTGTACTATAAAGATGTTAAGA	245	
Db	240	TTAATCAGTGGACGCT--GCCATGACTGGAATATGTTTCTACTCTCAAAACTGTTAAGA	296	

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 06:14:34 ; Search time 931.765 Seconds
(without alignments)
695.261 Million cell updates/sec

Title: US-10-010-731-14
Perfect score: 244
Sequence: 1 AHCENLANTYRGPCGCGCFHCKTKEHLISGRCDPRCC 40

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n model -DEV=xih
-Q/cgn2_1/USFTO.spool/US10010731/runat_17062003_095705_28177/app_query.fasta.1.398
-DB=EST -QFMT=fastap -SUFFIX=ist -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR-US10010731.ecgn.1.1.2463.ernat.17062003.095705.28171 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEIOBERRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: em_estda:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	75.8	446	9	AJ498901
2	184	75.4	426	12	BG838678
3	181	74.2	487	13	B1321179
4	162	66.4	517	9	AJ308155
5	145.5	59.6	574	14	B0151477
6	132.5	54.3	503	12	BF633403
7	118	48.4	438	13	B1642738
8	116	47.5	366	13	B1321308
9	77	31.6	238	13	B1642792
10	76.5	31.4	1087	17	CNS05E63
11	75.5	30.9	369	9	AJ499268
12	74.5	30.5	528	12	BE942973
13	74.5	30.5	548	9	AL367974
14	74.5	30.5	548	10	AM585761
15	74.5	30.5	596	12	BF645101
16	74.5	30.5	605	12	BF649943
17	74.5	30.5	650	12	BF647513
18	74.5	30.5	654	12	BF645260
19	74.5	30.5	658	12	BF649855
20	74.5	30.5	662	12	BF650421
21	73.5	30.1	217	14	T09323
22	72.5	29.7	261	9	AJ499675
23	72.5	29.7	262	9	AJ500483
24	72.5	29.7	292	10	AM203222
25	72.5	29.7	360	9	AJ474240
26	72.5	29.7	369	9	AJ499336
27	72.5	29.7	369	9	AJ499347
28	72.5	29.7	373	9	AJ499760
29	72.5	29.7	378	9	AJ502212
30	72.5	29.7	384	9	AJ500150
31	72.5	29.7	385	9	AJ500594
32	72.5	29.7	386	9	AJ500674
33	72.5	29.7	418	10	AV721256
34	72.5	29.7	420	9	AJ474375
35	72.5	29.7	420	9	AJ474376
36	72.5	29.7	424	14	B0661645
37	72.5	29.7	427	13	BM369664
38	72.5	29.7	427	13	BM377547
39	72.5	29.7	442	9	AJ499945
40	72.5	29.7	449	9	AJ499841
41	72.5	29.7	450	9	AJ499952
42	72.5	29.7	451	13	BM369646
43	72.5	29.7	454	9	AJ500390
44	72.5	29.7	458	9	AL383816
45	72.5	29.7	463	9	AJ499925

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AJ498901	LOCUS	AJ498901 MYPOSE Medicago truncatula cDNA clone mt--acc95209h10, mRNA sequence.	446 bp	EST 09-AUG-2002			
AJ498901	ACCESSION	AJ498901	GI:22089344				
AJ498901	VERSION	AJ498901.1	GI:22089344				
AJ498901	KEYWORDS	EST.					
AJ498901	SOURCE	barrel medic.					
AJ498901	ORGANISM	Medicago truncatula					
AJ498901		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.					
AJ498901	REFERENCE	1 (bases 1 to 446)					

AUTHORS Firtnhaber, C., Bartelsmeier, V., Meyer, F., Bartels, D., Bekel, T., Linke, B., Puhler, A. and Kuester, H.
TITLE Determination of transcript sequences from developing pods including seeds of Medicago truncatula genotype A17
JOURNAL Unpublished (2002)
COMMENT Contact: Kuester, H. Lehrstuhl fuer Genetik Universitaet Bielefeld Postfach 100131, D-33501 Bielefeld, Germany.
FEATURES Location/Qualifiers
 source
 1..446
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="mt-acc95209h10"
 /clone_11b="MPOSE"
 /tissue-type="pods including seeds"
 /dev_stage="different stages of development"
 /note="Vector: pGEM-T; Site_1: pGEM-T; Site_2: SphI; genotype A17; cDNA was prepared from polyA+ enriched RNA from developing pods including seeds harvested at different stages of development. The cDNA was directionally ligated by Medionomix into the pGEM-T vector from Promega using GCATCGCGCGCGCGCGCGCATG and CTCGAGCCATTATGCGCGG adapters. Plasmids containing cDNA inserts were propagated in E. coli DH10B cells."
BASE COUNT 147 a 84 c 83 g 132 t
ORIGIN
 Alignment Scores:
 Pred. No.: 1.69e-15 Length: 446
 Score: 185.00 Matches: 30
 Percent Similarity: 86.84% Conservative: 3
 Best Local Similarity: 78.95% Mismatches: 5
 Query Match: 75.82% Indels: 0
 DB: 9 Gaps: 0
 US-10-010-731-14 (1-40) x AJ498901 (1-446)
QY 2 ThcYsglunsluenaalaasnthrtyfargllyprocysphecglycysasphehis 21
 |||||
Db 145 ACTTGAGAAATTTGGCTGATTAATACAGGGGACCATCTTATGTTGTGTGATACAC 204
 |||||
QY 22 CyslysthrlysgluhisleuSerGlyArgcysargaspheargCys 39
 |||||
Db 205 TGCACACCAAGAGATGCAATGACGCGGAGGATGACATTCGTTG 258
 |||||
RESULT 2
LOCUS BG838678 426 bp mRNA linear EST 25-MAY-2001
DEFINITION GC01_03f01_A GC01_AAFc_ECORC_cold_stressed_glycine_clandestina
ACCESSION BG838678
VERSION BG838678.1 GI:14204985
KEYWORDS EST.
SOURCE Glycine clandestina
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 426)
AUTHORS Singh, J.A., Farah, S., Chapados, J., Courroux, P., De Moors, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Glycine clandestina Seedlings
JOURNAL Unpublished (2001)
COMMENT Contact: Singh, J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-Food Canada KM Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada
 Tel: (613) 759-1662

FEATURES Fax: (613) 759-1701
 Email: singhja@em.agr.ca.
SOURCE Location/Qualifiers
 1..426
 /organism="Glycine clandestina"
 /cultivar="1035"
 /db_xref="taxon:45687"
 /clone="GC01_03f01"
 /clone_11b="GC01_AAFc_ECORC_cold_stressed_glycine_clandestina"
 /tissue-type="leaves, stem"
 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI; Site_2: XhoI; Plants incubated at 2 degrees under 12 hours of light/day. Harvested after only 2-3 days of cold treatment. cDNA was prepared with the Uni-Zap cDNA kit from Stratagene. Eco RI adapters were linked followed by digest with Xho I/Eco RI and ligated to pBluescript."
BASE COUNT 116 a 92 c 86 g 125 t
ORIGIN
 Alignment Scores:
 Pred. No.: 2.18e-15 Length: 426
 Score: 184.00 Matches: 33
 Percent Similarity: 84.62% Conservative: 0
 Best Local Similarity: 84.62% Mismatches: 4
 Query Match: 75.41% Indels: 2
 DB: 12 Gaps: 1
 US-10-010-731-14 (1-40) x BG838678 (1-426)
QY 2 ThcYsglunsluenaalaasnthrtyfargllyprocysphecglycysasphehis 19
 |||||
Db 316 ACTTGAGAAACCTGGCTAATACATACAGGGGCGCATCTTACTACCGCAGCTGCAT 257
 |||||
QY 20 PhehisCyslysthrlysgluhisleuSerGlyArgcysargaspheargCys 38
 |||||
Db 256 GATCAGCTCAAGATAAAGAACTTACTCAGCGGAGTGACAGCAVATTTCCG 200
 |||||
RESULT 3
LOCUS B1321179 487 bp mRNA linear EST 29-NOV-2001
DEFINITION sat48610.y3 Gm-cl077 glycine max cDNA clone GENOME SYSTEMS CLONE
 ID: Gm-cl077-1723 5, similar to SW:10KD-VIGUN P18646 10 KD PROTEIN
 PRECURSOR ; mRNA sequence.
ACCESSION B1321179
VERSION B1321179.1 GI:15000365
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
REFERENCE 1 (bases 1 to 487)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 putative full length read
 vector to vector length is This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801
 For further information call: (800)-533-4363 or contact via email:

ccu@resgen.com
Seq primer: -40RP from Glibco
High quality sequence stop: 432.
Location/Qualifiers

1..487
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl077-1723"
/clone_id="Gm-cl077"
/tissue_type="18 day old 'Williams' seedlings"
/dev_stage="18 day old 'Williams' seedlings"
/lab_host="DH108"

/note="Vector: pBluescript II SK+; Site-1: EcoRI; Site-2: XhoI; The mRNA was isolated from cotyledons of 18-day-old 'Williams' seedlings which were greenhouse grown in liquid nitrogen. The cotyledons were flash-frozen in liquid nitrogen. Stratiagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratiagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGACTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adaptors and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (400/u1); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratiagene's pBluescript II XR predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratiagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."

BASE COUNT 152 a 96 c 102 g 137 t
ORIGIN

Alignment Scores:
Pred. No.: 6,71e-15 Length: 487
Score: 181.00 Matches: 32
Percent Similarity: 82.50% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 5
Query Match: 74.18% Indels: 2
DB: 13 Gaps: 1

US-10-010-731-14 (1-40) x B1321179 (1-487)

Oy 2 Thrcysgluasnleuulaasntrhrryarglyprocysphe-----glyglycysasp 19
Db 155 ACTTGGAGAACCTGGCTGATACATACAGGGGTCACATGCTTCCACCACTGGCAGCTGGCAT 214
Oy 20 Phehiscyslysthrlysgluhislleuleuserglyargcysargapasphearcys 39
Db 215 GATTCTGCAAGAACAAAGAGACACTTGCCTCAGAGGCGAGATGACGAGCGATTTTCGCTGT 274

RESULT 4
AJ308155 517 bp mRNA linear EST 29-OCT-2001
LOCUS AJ308155 SSH Pisum sativum cDNA clone PSSSH1clone91, mRNA sequence.
ACCESSION AJ308155
VERSION AJ308155.1 GI:16507870
KEYWORDS EST.
SOURCE pea.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 517)
AUTHORS Grunwald U., Lapopin L., Becker A., Mann P., Bomanskie N., Gianluigi Pearson V., and Franken P.
TITLE Screening for genes activated in Pisum sativum mycorrhiza by arbuscule development-related expression profiling
JOURNAL Unpublished (2001)
COMMENT Contact: Franken P
Biochemistry
Max-Planck-Institute for Terrestrial Microbiology
Marburg, Karl-von-Frisch-Strasse, D-35043, Germany.
Location/Qualifiers

FEATURES
source

1..517
/organism="Pisum sativum"
/cultivar="finale"
/db_xref="taxon:3888"
/clone="PSSSH1clone91"
/clone_id="SSH"
/tissue_type="arbuscular mycorrhiza"
/note="minus inoculated late mutant"

BASE COUNT 161 a 87 c 102 g 167 t
ORIGIN

Alignment Scores:
Pred. No.: 2.93e-12 Length: 517
Score: 162.00 Matches: 27
Percent Similarity: 77.50% Conservative: 4
Best Local Similarity: 67.50% Mismatches: 2
Query Match: 66.39% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x AJ308155 (1-517)

Oy 2 Thrcysgluasnleuulaasntrhrryarglyprocysphe-----glyglycysasp 19
Db 162 ACTTGGAGAACCTGGCTGATACATACAGGGGTCACATGCTTCCACCACTGGCAGCTGGCAT 221
Oy 20 Phehiscyslysthrlysgluhislleuleuserglyargcysargapasphearcys 39
Db 222 AACATTGCAAGAACAAAGAGACACTTGCCTCAGTGGAGGCTCAGGATGATTTTCGCTGC 281

RESULT 5
B0151477 574 bp mRNA linear EST 24-APR-2002
LOCUS B0151477
DEFINITION NF088A06.F1P1038 Developing leaf Medicago truncatula cDNA clone
ACCESSION NF088A06.F1P1038
VERSION B0151477
KEYWORDS GI:20288536
EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.

REFERENCE 1 (bases 1 to 574)
AUTHORS Torres-Jerez I., Scott A.D., Harris A.R., Gonzales R.A., Bell C.J., Flores H.R., Imman J.T., Weller J.W. and May G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert length: 574 Std Error: 0.00
Plate: 068 Row: A Column: 06
Seq primer: TCACACAGAAACAGCTATGAC.

BASE COUNT	63 a	60 c	49 g	60 t	6 others
ORIGIN					
Alignment Scores:					
Pred. No.:	0.483	Length:	238		
Score:	77.00	Matches:	19		
Percent Similarity:	58.33%	Conservative:	2		
Best Local Similarity:	52.78%	Mismatches:	12		
Query Match:	31.56%	Indels:	3		
Ds:	13	Gaps:	1		
US-10-010-731-14 (1-40) x B1642792 (1-238)					
Oy	1 AAlrPhrCyGSjuaNleuAlaSnThrTyArgGlyProCySpHe-----GlyGlyCys 18				
Db	132 TCgACTTCGGAACCGCTGGCTGCTACATTCAGGGGCTTATCCATTCACCTGTGCTACATCGC 191				
Oy	19 ASpHeHtScys-LysThrTyGSjuaHtSleuLeuSerGlyArgCys 33				
Db	192 GACGATCATCTGCNNMGACATATATATCTTACTCTCAGTCCACGATGC 237				
RESULT 10					
CNS05E63	1087 bp DNA linear GSS 26-MAY-2000				
LOCUS	CNS05E63				
DEFINITION	Tetraodon nigroviridis genome survey sequence, T7 end of clone 017C04 of library A from Tetraodon nigroviridis, genomic survey sequence.				
ACCESSION	AL333300				
VERSION	AL333300.1 GI:8227058				
KEYWORDS	GSS: genome survey sequence.				
SOURCE	Tetraodon nigroviridis.				
ORGANISM	Tetraodon nigroviridis				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.				
REFERENCE	1 (bases 1 to 1087)				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.				
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1087)				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Fitzames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.				
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 1087)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-APR-2000)				
COMMENT	This sequence is a single read and was generated as part of a large scale clone end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .				
FEATURES	Location/Qualifiers				
source	1..1087				
	/organism="Tetraodon nigroviridis"				
	/db_xref="taxon:99883"				
	/clone="017C04"				
	/clone_1bp="A"				
	/note="Genoscope sequence ID : C0NA017B802C1-end : T7"				
BASE COUNT	301 a	231 c	276 g	266 t	13 others
ORIGIN					
Alignment Scores:					
Pred. NO.:	4.16	Length:	1087		
Score:	76.50	Matches:	16		
Percent Similarity:	45.24%	Conservative:	3		
Best Local Similarity:	38.10%	Mismatches:	14		

Query Match:	31.35%	Indels:	9
DB:	17	Gaps:	2
US-10-010-731-14 (1-40) x CNS05E63 (1-1087)			
OY	4	GlusnlsnleuAlaAsnPTTATrArgG1}ProCys-----PheG1yG1Cys	18
Db	880	GAGTTMAGCCANACACATACAGAGACCTTTGATGGTGTACACGGGATATGATGGTGT	939
OY	19	AspRheniscysLysrHrLysGlnHlsleuLeuSerG1yATrGysATrGAspAspPheArg	38
Db	940	ACTTAACACACACACACACACACACAGTACACACAGAAATGT-----TCA	987
OY	39	CysCys	40
Db	988	TGTTGC	993
RESULT 11			
LOCUS	AJ499268	369 bp	mRNA linear EST 09-AUG-2002
DEFINITION	AJ499268 MTGIM Medicago truncatula cDNA clone mtgmacc120002b01,		
ACCESSION	AJ499268		
VERSION	AJ499268.1		
KEYWORDS	GI:22089711		
SOURCE	EST.		
ORGANISM	barrel medic.		
	Medicago truncatula		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;		
	Medicago.		
REFERENCE	1 (bases 1 to 369)		
AUTHORS	Krajinski,F., Manthey,K., Bartelsmeier,V., Meyer,F., Bartels,D.,		
	Bekel,T., Linke,B., Franken,P., Kuester,H., Perlick,A.M. and		
	Puehler,A.		
TITLE	Detection of transcript sequences from mycorrhizal roots of the		
	model mycorrhiza Medicago truncatula genotype A17 - Glomus		
	intraradices using the approach of an EST genome project based on		
	an SSH library		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Krajinski F		
	LG Molekulargenetik		
	Herrnhaeuser Str. 2 D-30419 Hannover, Germany.		
FEATURES	Location/Qualifiers		
source	1..369		
	/organism="Medicago truncatula"		
	/db_xref="taxon:3880"		
	/clone="mtgmacc120002b01"		
	/clone_id="MTGIM"		
	/lssue_type="mycorrhizal roots"		
	/dev_stage="3 weeks after inoculation"		
	/note="Vector: pGEM-Teasy; genotype A17; cDNA was prepared		
	from total RNA using the SMART PCR cDNA system (Clontech)		
	from roots harvested three weeks after inoculation with		
	Glomus intraradices. This cDNA was used as tester in a		
	Suppression Subtractive Hybridization (SSH). The SSH-cDNA		
	fragments were generated using the SSH-adaptor sequences		
	ctatagcactcaatagagctcgagcgagcgagcgagcgagcgagct and		
	ctatagcactcaatagagcgagcgagcgagcgagcgagcgagct (Clontech) and		
	ligated after Suppression Subtractive Hybridization in to		
	the pGEM-Teasy vector from Promega. Plasmids containing		
	cDNA inserts were propagated in E. coli TOP 10F' cells		
	(Invitrogen)"		
BASE COUNT	125 a	53 c	69 g
ORIGIN			122 t
Alignment Scores:			
Pred. No.:	1.38	Length:	369
Score:	75.50	Matches:	15
Percent Similarity:	45.24%	Conservative:	4
Best Local Similarity:	35.71%	Mismatches:	18
Query Match:	30.94%	Indels:	5
DB:	9	Gaps:	2

Best Local Similarity: 38.10% Mismatches: 19
 Query Match: 30.53% Indels: 5
 DB: 9 Gaps: 2

US-10-010-731-14 (1-40) x AL367974 (1-548)

QY 3 CysGluAsnLeuAlaAsnThrTyrArgGlyProCysPhe-----GlyGlyCysAspPhe 20

DB 287 TGTGAAGGCGAAGCAAAACATGTCAGACCTTGCTTATCTCAGCAAAATGTAAAGA 228

QY 21 HisCysIsthrLysGluHisLeuSerGlyArgCysArgAspAsp-----Phe 37

DB 227 CAGTGCATCAATGTTGAGCATGCAACTTGTGCTTGTCCACCGTCAGGCAATGCTTTT 168

QY 38 ArgCys 39

DB 167 GCCTGC 162

RESULT 14

AM585761 548 bp mRNA linear EST 07-SEP-2000

LOCUS ESTJ17364 MHAM Medicago truncatula/Gloms versiforme mixed EST

ACCESSION library CDNA clone pMHAM-39M12, mRNA sequence.

VERSION AM585761.1 GI:7265275

KEYWORDS Medicago truncatula/Gloms versiforme mixed EST library.

SOURCE Eukaryota; mixed EST libraries.

REFERENCE 1 (bases 1 to 548)

AUTHORS Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,

Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.

ESTs from roots of Medicago truncatula after colonization with

Gloms versiforme

JOURNAL Unpublished (2000)

COMMENT Contact: Maria J. Harrison

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73401, USA

Tel: 580-223-5810

Fax: 580-221-7380

Email: mjharrison@noble.org

Noble EST name: N254689e

TIGR sequence name: MDAF78TK

More information is available at: 'http://chrysis.tamu.edu/medicago'

Seq primer: Skmod (CTA GAA CTA gtg. gat CC).

Location/Qualifiers

1. 348

/organism="Medicago truncatula/Gloms versiforme mixed EST

library"

/db_xref="taxon:119092"

/clone="PMHAM-39M12"

FEATURES

source

1. 596

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF034G12EC"

/tissue_type="Elicited cell culture"

/dev_stage="Cell suspensions were subcultured every 14

days. Cells were induced six days after subculture"

/note="Vector: Lambda Zap; Cells were induced with yeast

cell wall extracts equivalent to 50ug/ml glucose in the

final concentration. Samples were taken at 0.5, 1, 12 and

24 hours after induction. Equal amounts of RNA from each

time point were pooled and used for mRNA isolation."

Pred. No.: 3.18 Length: 548

Score: 74.50 Matches: 16

Percent Similarity: 42.86% Conservative: 2

Best Local Similarity: 38.10% Mismatches: 19

Query Match: 30.53% Indels: 5

DB: 10 Gaps: 2

US-10-010-731-14 (1-40) x AM585761 (1-548)

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DB 273 TGTGAAGGCGAAGCAAAACATGTCAGACCTTGCTTATCTCAGCAAAATGTAAAGA 332

QY 21 HisCysIsthrLysGluHisLeuSerGlyArgCysArgAspAsp-----Phe 37

DB 333 CAGTGCATCAATGTTGAGCATGCAACTTGTGCTTGTCCACCGTCAGGCAATGCTTTT 392

QY 38 ArgCys 39

DB 393 GCCTGC 398

RESULT 15

BF645101

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 596 Std Error: 0.00

Plate: 034 row: G column: 12

Seq primer: TCACACAGCAACACGCTATGAC.

Location/Qualifiers

1. 596

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF034G12EC"

/tissue_type="Elicited cell culture"

/dev_stage="Cell suspensions were subcultured every 14

days. Cells were induced six days after subculture"

/note="Vector: Lambda Zap; Cells were induced with yeast

cell wall extracts equivalent to 50ug/ml glucose in the

final concentration. Samples were taken at 0.5, 1, 12 and

24 hours after induction. Equal amounts of RNA from each

time point were pooled and used for mRNA isolation."

Pred. No.: 3.56 Length: 596

Score: 74.50 Matches: 16

Percent Similarity: 42.86% Conservative: 2

Best Local Similarity: 38.10% Mismatches: 19

Query Match: 30.53% Indels: 5

DB: 10 Gaps: 2

US-10-010-731-14 (1-40) x AM585761 (1-548)

QY 3 CysGluAsnLeuAlaAsnThrTyrArgGlyProCysPhe-----GlyGlyCysAspPhe 20

DB 273 TGTGAAGGCGAAGCAAAACATGTCAGACCTTGCTTATCTCAGCAAAATGTAAAGA 332

QY 21 HisCysIsthrLysGluHisLeuSerGlyArgCysArgAspAsp-----Phe 37

DB 333 CAGTGCATCAATGTTGAGCATGCAACTTGTGCTTGTCCACCGTCAGGCAATGCTTTT 392

QY 38 ArgCys 39

DB 393 GCCTGC 398

RESULT 15

BF645101

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 596 Std Error: 0.00

Plate: 034 row: G column: 12

Seq primer: TCACACAGCAACACGCTATGAC.

Location/Qualifiers

1. 596

/organism="Medicago truncatula"

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/clone="NF034G12EC"

/tissue_type="Elicited cell culture"

/dev_stage="Cell suspensions were subcultured every 14

days. Cells were induced six days after subculture"

/note="Vector: Lambda Zap; Cells were induced with yeast

cell wall extracts equivalent to 50ug/ml glucose in the

final concentration. Samples were taken at 0.5, 1, 12 and

24 hours after induction. Equal amounts of RNA from each

time point were pooled and used for mRNA isolation."

BASE COUNT

ORIGIN

Alignment Scores:

Best Local Similarity:

Query Match: 30.53% Indels: 5
DB: 12 Gaps: 2

US-10-010-731-14 (1-40) x BF645101 (1-596)

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QY	21	HisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAsp-----Phe	37
Db	337	CAGTGCATCAATGTTGAGCATGCAACTTCTGCTGCTCACCCTCAAGGCATTGGTTT	396
QY	38	ArgCys	39
Db	397	GCTTGC	402

Search completed: June 21, 2003, 07:52:33
Job time : 934.765 secs

~~BEST AVAILABLE COPY~~

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 06:15:24 ; Search time 31.5294 Seconds
(without alignments)
389.068 Million cell updates/sec

Title: US-10-010-731-14

Perfect score: 244

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	244	100.0	293	3	US-08-766-355-6
2	244	100.0	293	4	US-09-003-198A-6
3	244	100.0	293	4	US-09-428-805-6
4	194	79.5	189	4	US-09-003-198A-18
5	194	79.5	200	3	US-08-766-355-5
6	194	79.5	200	4	US-09-003-198A-5
7	194	79.5	200	4	US-09-428-805-5
8	185	75.8	250	4	US-08-766-355-13
9	185	75.8	250	4	US-09-003-198A-13
10	185	75.8	250	4	US-09-428-805-13
11	185	75.8	490	4	US-09-003-198A-19
12	185	75.8	507	3	US-08-766-355-10

13	185	75.8	507	4	US-09-003-198A-10	Sequence 10, Appl
14	185	75.8	507	4	US-09-428-805-10	Sequence 9, Appl
15	171	70.1	327	3	US-08-766-355-9	Sequence 10, Appl
16	171	70.1	327	4	US-09-003-198A-9	Sequence 9, Appl
17	171	70.1	327	4	US-09-428-805-9	Sequence 35, Appl
18	162	66.4	141	1	US-08-377-687-35	Sequence 35, Appl
19	162	66.4	141	1	US-08-771-192-35	Sequence 35, Appl
20	162	66.4	141	1	US-08-971-982-35	Sequence 15, Appl
21	63	3777	3	4	US-09-121-121-15	Sequence 15, Appl
22	63	3777	4	4	US-08-933-803A-15	Sequence 2, Appl
23	62.5	25.6	4403765	4	US-09-103-840A-2	Sequence 1, Appl
24	62.5	25.6	4411529	4	US-09-103-840A-1	Sequence 36, Appl
25	62	25.4	147	1	US-08-377-687-36	Sequence 36, Appl
26	62	25.4	147	1	US-08-777-192-36	Sequence 36, Appl
27	62	25.4	147	4	US-08-971-982-36	Sequence 31, Appl
28	62	25.4	150	1	US-08-377-687-31	Sequence 31, Appl
29	62	25.4	150	1	US-08-777-192-31	Sequence 31, Appl
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33	61	25.0	4403765	4	US-09-103-840A-2	Sequence 1, Appl
34	61	25.0	4411529	4	US-09-103-840A-1	Sequence 1, Appl
35	59	24.2	3460	2	US-08-751-305-1	Sequence 17, Appl
36	58	23.8	1356	4	US-09-134-001C-617	Sequence 6, Appl
37	58	23.8	2274	4	US-09-388-743-17	Sequence 3, Appl
38	57.5	23.6	383	4	US-09-122-400B-3	Sequence 6, Appl
39	56.5	23.2	363	1	US-08-543-238-6	Sequence 6, Appl
40	56.5	23.2	363	1	US-08-420-526-6	Sequence 4, Appl
41	56.5	23.2	492	1	US-08-543-238-4	Sequence 4, Appl
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ALIGNMENTS

RESULT 1
US-08-766-355-6
Sequence 6, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
zip: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

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; INFORMATION FOR SEQ ID NO: 6:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 293 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
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; FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: one-of(17, 265)
;   OTHER INFORMATION: /mod_base= OTHER
;
; OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-6

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Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             3           Gaps:          0

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QY      21 HisCysLysThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCysCys 40
DB      233 CACTGCAAAACCAAGACACTTACTTAGCGGNAGGTGCGAGGACGACTTCCGCTGCTGC 292

RESULT 2
US-09-003-198A-6
; Sequence 6, Application US/09003198A
; Patent No. 6316407
;
; GENERAL INFORMATION:
;   APPLICANT: Liang, Jihong
;   APPLICANT: Shah, Dilip Meganalal
;   APPLICANT: Wu, Yonnie S.
;   APPLICANT: Rosenberger, Cindy A.
;   APPLICANT: Hakimi, Salim
;
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;   NUMBER OF SEQUENCES: 19
;   CONTROLLING Plant Pathogenic Fungi
;
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77210
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/003,198A
;   FILING DATE: 07-JAN-1998
;
; CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Paterson, Melinda L.
;     REGISTRATION NUMBER: 33,062
;     REFERENCE/DOCKET NUMBER: MOBT:193
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (713) 787-1400
;     TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 293 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear

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; FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: one-of(17, 265)
;   OTHER INFORMATION: /mod_base= OTHER
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; OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-003-198A-6

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QY      21 HisCysLysThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCysCys 40
DB      233 CACTGCAAAACCAAGACACTTACTTAGCGGNAGGTGCGAGGACGACTTCCGCTGCTGC 292

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US-09-428-805-6
; Sequence 6, Application US/09428805
; Patent No. 6329504
;
; GENERAL INFORMATION:
;   APPLICANT: Liang, Jihong
;   APPLICANT: Shah, Dilip Meganalal
;   APPLICANT: Wu, Yonnie S.
;   APPLICANT: Rosenberger, Cindy A.
;   APPLICANT: Hakimi, Salim
;
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;   NUMBER OF SEQUENCES: 14
;   CONTROLLING Plant Pathogenic Fungi
;
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 77210
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: United States of America
;   ZIP: 77210
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/428,805
;   FILING DATE:
;
; CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/766,355
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Kitchell, Barbara S.
;     REGISTRATION NUMBER: 33,928
;     REFERENCE/DOCKET NUMBER: MOBT:063
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (512) 418-3000
;     TELEFAX: (512) 474-7577
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 293 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;   FEATURE:
;     NAME/KEY: modified_base
;     LOCATION: one-of(17, 265)

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; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-428-805-6

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Pred. No.: 1,7e-25 Length: 293
Score: 244.00 Matches: 40
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US-10-010-731-14 (1-40) x US-09-428-805-6 (1-293)

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QY 21 HisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCysCys 40
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Db 233 CACTGCAAAACCAAGAACACTTACTTAGCGGNAAGTGCAGGGACGACTTCCGCTGCTGC 292

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; Sequence 18, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Meganalal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-003-198A-18

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Best Local Similarity: 79.49% Mismatches: 5
Query Match: 79.51% Indels: 0
DB: 4 Gaps: 0
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Db 126 TGCAACACCAAGAACGACGACTTAGTGAAGGTGTAGGACGACTTCCGCTGCTGC 182

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; Sequence 5, Application US/08766355
; Patent No. 6121436
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Meganalal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,355
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 474-7577
; TELEFAX: (512) 418-3000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
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; NAME/KEY: modified_base
; LOCATION: 17
; OTHER INFORMATION:
; OTHER INFORMATION: /mod_base= OTHER
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Best Local Similarity: 79.49% Mismatches: 5
Query Match: 79.51% Indels: 0
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APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-428-805-13

Alignment Scores:
Pred. No.: 1.94e-17 Length: 250
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-14 (1-40) x US-09-428-805-13 (1-250)

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Db 108 ACATGTGAGAAATTGGCAGATAATATAGGGACCATGCTTTAGTGTGTGACACTCAC 167

QY 22 Cyslysthrlysluhtleuuserglyargcysargaspasppheargcys 39
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Db 168 TGCACAACCAAGAGAACGCGATTAGTGAAGCTGTAGGACGACTCCGCTGC 221

RESULT 11

US-09-003-198A-19
Sequence 19, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
OPERATING SYSTEM: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-003-198A-19

Alignment Scores:
Pred. No.: 4.54e-17 Length: 490
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-14 (1-40) x US-09-003-198A-19 (1-490)

QY 2 Thrcysgluasneulaasnthrtyrarglyprocysphedglycysasppheh1s 21
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Db 159 ACATGTGAGAAATTGGCAGATAATATAGGGACCATGCTTTAGTGTGTGACACTCAC 218

QY 22 Cyslysthrlysluhtleuuserglyargcysargaspasppheargcys 39
||| |||||
Db 219 TGCACAACCAAGAGAACGCGATTAGTGAAGCTGTAGGACGACTCCGCTGC 272

RESULT 12

US-08-766-355-10
Sequence 10, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
OPERATING SYSTEM: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)

OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-10

Alignment Scores:
Pred. No.: 4,74e-17 Length: 507
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 3 Gaps: 0

US-10-010-731-14 (1-40) x US-08-766-355-10 (1-507)

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QY 22 CysLysThrlsGlnHisLeuSergLYrGysArgAspAspPheArgCys 39
|||
DB 236 TGCACAACCAAGAGAACCGCAGTTAGTGAAGGTGTAGGACACACTCCGCTGC 289
|||

RESULT 13
US-09-003-198A-10
Sequence 10, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakiml, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-003-198A-10

Alignment Scores:
Pred. No.: 4,74e-17 Length: 507
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 3 Gaps: 0

Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-14 (1-40) x US-09-003-198A-10 (1-507)

QY 2 ThrcysgluasnlleuAlaasnThrTYrArgGLyProCyspHegLyGLyCysaspPheHs 21
|||||
DB 176 ACATGTGAGAAATTTGGCAGATTAATATAGGGACCATGCTTTAGTGTGTTGACACTCAC 235
|||||

QY 22 CysLysThrlsGlnHisLeuSergLYrGysArgAspAspPheArgCys 39
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DB 236 TGCACAACCAAGAGAACCGCAGTTAGTGAAGGTGTAGGACACACTCCGCTGC 289
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RESULT 14
US-09-428-805-10
Sequence 10, Application US/09428805
Patent No. 6329504
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakiml, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-428-805-10

Alignment Scores:
Pred. No.: 4,74e-17 Length: 507
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 4 Gaps: 0

Query Match: 75.82% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-14 (1-40) x US-09-428-805-10 (1-507)

QY 2 ThcYsgGlUhsLeuLeuSerGlyArgCysArgAspPheHis 21
|||||
DB 176 ACATGTGAGAAATTGGCAGATTAATATAGGGACCATGCTTAGTGTGTGACACATCAG 235
|||||

QY 22 CysLygThrlYsgLhUhsLeuLeuSerGlyArgCysArgAspPheArgCys 39
|||
DB 236 TGCACACACAGAACAGACGAGTTAGTGGAGGTGAGGACGACCTTCGCTGC 289
|||||

RESULT 15

US-08-766-355-9

; Sequence 9, Application US/08766355

; Patent No. 6121436

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip Maganlal

; APPLICANT: Wu, Yonnie S.

; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; NUMBER OF SEQUENCES: 14 Controlling Plant Pathogenic Fungi

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 77210

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,355

; FILING DATE: Concurrently Herewith

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Kilchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: MOBT:063

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 327 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: one-of(244, 305)

; OTHER INFORMATION: /mod_base= OTHER

; OTHER INFORMATION: /note= "N = A or C or G or T"

US-08-766-355-9

Alignment Scores:

Pred. No.: 2,34e-15

Score: 171.00

Percent Similarity: 86.11%

Best Local Similarity: 77.78%

Query Match: 70.08%

DB: 3

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DB 1 GAGAAATTTGGCGGATAGTATAGCGGACCATGCTTAGTGTGTGACACTCAGTCAGCA 60
|||||

QY 24 ThrlYsgLhUhsLeuLeuSerGlyArgCysArgAspPheArgCys 39
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DB 61 ACCAAAGAGAACGCGAGTTAGTGAAGGTGAGGATGACTTTCGTTGT 108
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 07:19:24 ; Search time 97.8824 Seconds
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Title: US-10-010-731-14

Perfect score: 244
Sequence: 1 ATCENMANTYRSGPCFGCGDHFCKTREHLISGRCDRFRCC 40

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Searched: 1042519 seqs, 733713590 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	199	81.6	461	9	US-10-178-213-451
3	194	79.5	189	9	US-10-010-731-18
4	194	79.5	200	9	US-10-010-731-5

5	190	77.9	494	9	US-09-805-694B-5	Sequence 5, Appl1
6	185	75.8	250	9	US-10-010-731-13	Sequence 13, Appl1
7	185	75.8	490	9	US-10-010-731-19	Sequence 19, Appl1
8	185	75.8	507	9	US-10-010-731-10	Sequence 10, Appl1
9	183.5	75.2	420	9	US-10-178-213-436	Sequence 436, App
10	183	75.0	563	9	US-10-178-213-439	Sequence 439, App
11	171	70.1	327	9	US-10-010-731-9	Sequence 9, Appl1
12	162	66.4	141	10	US-09-759-584-35	Sequence 379, App
13	140	57.4	464	9	US-10-178-213-379	Sequence 100, App
14	85.5	35.0	471	9	US-10-178-213-100	Sequence 106, App
15	80.5	33.0	441	9	US-10-178-213-106	Sequence 103, App
16	80	32.8	534	9	US-10-178-213-103	Sequence 97, Appl
17	75	30.7	468	9	US-10-178-213-97	Sequence 340, App
18	72.5	29.7	553	9	US-10-178-213-340	Sequence 403, App
19	72	29.5	573	9	US-10-178-213-403	Sequence 13068, A
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21	71.5	29.3	272	10	US-09-878-574-10791	Sequence 11794, A
22	71.5	29.3	277	10	US-09-878-574-11794	Sequence 1139, Ap
23	71.5	29.3	361	10	US-09-878-574-1139	Sequence 343, App
24	71.5	29.3	445	9	US-10-178-213-343	Sequence 334, App
25	71.5	29.3	459	9	US-10-178-213-334	Sequence 527, App
26	71.5	29.3	2146	10	US-09-954-456-527	Sequence 1, Appl1
27	71.5	29.3	2146	10	US-09-842-307-1	Sequence 325, App
28	70.5	28.9	425	9	US-10-178-213-325	Sequence 331, App
29	70.5	28.9	587	9	US-10-178-213-331	Sequence 14296, A
30	69.5	28.9	275	10	US-09-878-574-14296	Sequence 385, App
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32	68.5	28.1	243	10	US-09-878-574-13309	Sequence 12979, A
33	67.5	27.7	246	10	US-09-878-574-12979	Sequence 15260, A
34	67.5	27.7	246	10	US-09-878-574-15260	Sequence 13640, A
35	67.5	27.3	257	10	US-09-878-574-13340	Sequence 427, App
36	66.5	27.3	264	10	US-09-878-574-13620	Sequence 409, App
37	66.5	27.3	338	9	US-10-178-213-427	Sequence 37, Appl
38	66.5	27.3	504	9	US-10-178-213-409	Sequence 2276, Ap
39	66.5	27.3	635	9	US-10-178-213-37	Sequence 283, App
40	65	26.6	73308	10	US-09-954-456-2276	Sequence 254, App
41	64	26.2	373	10	US-09-770-696-283	Sequence 337, App
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43	63.5	26.0	399	9	US-10-178-213-337	Sequence 19350, A
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ALIGNMENTS

RESULT 1
US-10-010-731-6
; Sequence 6, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Meghmal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001

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CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /mod_base= OTHER
/note= "N = A or C or G or T"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-010-731-6
Alignment Scores:
Pred. No.: 7.54e-28 Length: 293
Score: 244.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB 21 HlScyLysThrLysGluHlSleuSerGlyArgCysArgAspAspPheArgCys 40
233 CACTGCMAAACCAAGACACTTACTTAGCGGAGGTGCAGGACGACTTCCGCTGCTGC 292
RESULT 2
US-10-178-213-451
Sequence 451, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Hermann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 451
LENGTH: 461
TYPE: DNA
ORGANISM: Arabidopsis hypogaea
FEATURE:
NAME/KEY: CDS
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LOCATION: (44)...(271)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (128)...(268)
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NAME/KEY: misc.feature
LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451
Alignment Scores:
Pred. No.: 7.31e-21 Length: 461
Score: 199.00 Matches: 35
Percent Similarity: 87.80% Conservative: 1
Best Local Similarity: 85.37% Mismatches: 3
Query Match: 81.56% Indels: 2
DB: 9 Gaps: 1
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DB 19 AspPheHisCysLysThrLysGluHlSleuSerGlyArgCysArgAspAspPheArg 38
188 GACGACCACTGCMAAGCAAGGACACACTGCTCAGCGGCGCGCTCGGACGACTTCCGC 247
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DB 248 TGT 250
RESULT 3
US-10-010-731-18
Sequence 18, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakiml, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
```

```

; LENGTH: 189 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-010-731-18

Alignment Scores:
Pred. No.: 1,34e-20 Length: 189
Score: 194.00 Matches: 31
Percent Similarity: 87.18% Conservative: 3
Best Local Similarity: 79.49% Mismatches: 5
Query Match: 79.51% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-18 (1-189)

OY 2 ThrcysgluasnleualaasnThrTYrArgGlyProCysPheGlyGlyCysAspPheHis 21
Db 66 ACATGTGAGAAATTGGCAGATAAATATAGGGACCATGCTTATAGTGTTGTGACACTGCAC 125
OY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCysCys 40
Db 126 TGCACAACCAAGAGACGCGATTAGTGAAGGTGATGAGGACGACACTTCCGCTGCTGC 182

RESULT 4
US-10-010-731-5
; Sequence 5, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Mu, Yonnie S.
; Rosenberger, Cindy A.
; Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,731
; FILING DATE: 13-No. US20030041347A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/003,198
; FILING DATE: 07-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Paterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 17
```

```

; OTHER INFORMATION: /mod_base= OTHER
; /note= "N" = A or C or G or T"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-731-5

Alignment Scores:
Pred. No.: 1.44e-20 Length: 200
Score: 194.00 Matches: 31
Percent Similarity: 87.18% Conservative: 3
Best Local Similarity: 79.49% Mismatches: 5
Query Match: 79.51% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-5 (1-200)

OY 2 ThrcysgluasnleualaasnThrTYrArgGlyProCysPheGlyGlyCysAspPheHis 21
Db 83 ACATGTGAGAAATTGGCAGATAAATATAGGGACCATGCTTATAGTGTTGTGACACTGCAC 142
OY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCysCys 40
Db 143 TGCACAACCAAGAGACGCGATTAGTGAAGGTGATGAGGACGACACTTCCGCTGCTGC 199

RESULT 5
US-09-805-694B-5
; Sequence 5, Application US/09805694B
; Publication No. US20030041350A1
; GENERAL INFORMATION:
; APPLICANT: Kinney, Anthony
; TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
; FILE REFERENCE: B1432 US NA
; CURRENT APPLICATION NUMBER: US/09/805,694B
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,823
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (9)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (388)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (392)-(393)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (460)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (463)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: (468)
; LOCATION: (468)
; OTHER INFORMATION: n = A, C, G, or T
; OTHER INFORMATION: n = A, C, G, or T
US-09-805-694B-5

Alignment Scores:
Pred. No.: 1.78e-19 Length: 494
Score: 190.00 Matches: 33
Percent Similarity: 85.00% Conservative: 1
Best Local Similarity: 82.50% Mismatches: 4
Query Match: 77.87% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-09-805-694B-5 (1-494)

OY 2 ThrcysgluasnleualaasnThrTYrArgGlyProCysPhe-----GlyGlyCysAsp 19
```

Db 133 ACTTGCAGAACCTGGCTGATACATACAGGGGTCATGCTTACACACTGCGAGCTGCGAT 192
QY 20 PheHISCysLysThrLysGluHisLeuLeuSerClyArgCysArgAspPheArgCys 39
Db 193 GATCAGTCGCAAGAACAGACGACTTCTCAGAGCGCAGATGCGAGCGAGATTTTCGCTGT 252

RESULT 6

US-10-010-731-13
; Sequence 13, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:

APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440

INFORMATION FOR SEQ. ID NO: 13:
SEQUENCE CHARACTERISTICS:

LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ. ID NO: 13:

US-10-010-731-13

Alignment Scores:

Pred. No.: 4,24e-19 Length: 250
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-13 (1-250)

QY 2 ThCysGluAsnLeuAlaAsnThrTyArgGlyProCysPheGlyGlyCysAspPheHis 21

Db 108 ACATGTGAGAAATTGGCAGATAATATAGCGGACCATGCTTAGTGTTGTGACACTCAC 167

QY 22 CysLysThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCys 39

Db 168 TGCACACCAAGAACGACGATTAGTGAAGGTGAGGACGACACTTCCGCTGC 221

RESULT 7

US-10-010-731-19
; Sequence 19, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:

APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440

INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 490 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ. ID NO: 19:

US-10-010-731-19

Alignment Scores:

Pred. No.: 9.86e-19 Length: 490
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-19 (1-490)

QY 2 ThCysGluAsnLeuAlaAsnThrTyArgGlyProCysPheGlyGlyCysAspPheHis 21

Db 159 ACATGTGAGAAATTGGCAGATAATATAGCGGACCATGCTTAGTGTTGTGACACTCAC 218

QY 22 CysLysThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCys 39

Db 219 TGCACACCAAGAACGACGATTAGTGAAGGTGAGGACGACACTTCCGCTGC 272

RESULT 8

US-10-010-731-10

; Sequence 10, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:

APPLICANT: Liang, Jihong
Shah, Dilip Maganlal

```

1      Mu, Yonnie S.
2      Rosenberger, Cindy A.
3      Hakim, Salim
4      TITLE OF INVENTION: Antifungal Polypeptide And Methods for
5      Controlling Plant Pathogenic Fungi
6      NUMBER OF SEQUENCES: 19
7      CORRESPONDENCE ADDRESS:
8      ADDRESSEE: Arnold White & Durkee
9      STREET: P.O. Box 4433
10     CITY: Houston
11     STATE: Texas
12     COUNTRY: USA
13     ZIP: 77210
14
15     COMPUTER READABLE FORM:
16
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC-DOS/MS-DOS
20     SOFTWARE: Patent In Release #1.0, Version #1.30
21
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/10/010,731
24     FILING DATE: 13-No. US20030041347A1-2001
25
26     CLASSIFICATION: <Unknown>
27
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 09/003,198
30     FILING DATE: 07-JAN-1998
31
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Patterson, Melinda L.
34     REGISTRATION NUMBER: 33,062
35     REFERENCE/DOCKET NUMBER: MOBT:193
36
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: (713) 787-1400
39     TELEFAX: (713) 787-1440
40
41     INFORMATION FOR SEQ ID NO: 10:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 507 base pairs
44     TYPE: nucleic acid
45     STRANDEDNESS: double
46     TOPOLOGY: linear
47
48     FEATURE:
49     NAME/KEY: modified_base
50     LOCATION: one-of(17, 424, 485)
51     OTHER INFORMATION: /mod_base= OTHER
52     /note= "N = A or C or G or T"
53
54     SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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56     US-10-010-731-10
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1  APPLICANT: MCGutchen, Billy Fred
2  APPLICANT: Lu, Albert
3  APPLICANT: Hermann, Rafael
4  APPLICANT: Wong, James
5  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
6  FILE OF INVENTION: Use
7  FILE REFERENCE: 35718/246703
8  CURRENT APPLICATION NUMBER: US/10/178,213
9  PRIOR APPLICATION NUMBER: 60/300,152
10 PRIOR FILING DATE: 2001-06-22
11 PRIOR APPLICATION NUMBER: 60/300,241
12 PRIOR FILING DATE: 2001-06-22
13 NUMBER OF SEQ ID NOS: 469
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 436
16 LENGTH: 420
17 TYPE: DNA
18 ORGANISM: Cyamopsis tetragonoloba
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: (31)...(264)
22 FEATURE:
23 NAME/KEY: mat.peptide
24 LOCATION: (118)...(261)
25 US-10-178-213-436
26
27 Alignment Scores:
28 Pred. No.:
29 Score: 1.36e-18 Length: 420
30 Percent Similarity: 183.50 Matches: 32
31 Best Local Similarity: 85.378 Conservative: 3
32 Query Match: 78.058 Mismatches: 3
33 DB: 75.208 Indels: 1
34 Gaps: 1
35
36 US-10-010-731-14 (1-40) x US-10-178-213-436 (1-420)
37
38 QY 2 ThcCysgluAuaSleuAlaasnThrTyTyrArgIyProCysPheGlyGly-----Cys 18
39 Db 121 ACATGTCAGATCTTTCACAGATCATTCACAGGCGTCCATCTTCCCGAACCAGCCAGCTGC 186
40 QY 19 AspPheHisCysIysThrIySGluHisLeuSerGlyArgGcYargAspAspPhearg 38
41 Db 181 AACGATCTACTGCAAGAACACAAAGAGACCTTGCTCAGCGGAAGGTGCAGAGCATTTTCGC 240
42 QY 39 Cys 39
43 Db 241 TGC 243
44
45 RESULT 10
46 US-10-178-213-439
47 Sequence 439, Application US/10178213
48 Publication No. US20030041348A1
49
50 GENERAL INFORMATION:
51 APPLICANT: Simmons, Carl R.
52 APPLICANT: Navarro Acevedo, Pedro A.
53 APPLICANT: Harvell, Leslie
54 APPLICANT: Cahoon, Rebecca
55 APPLICANT: MCGutchen, Billy Fred
56 APPLICANT: Lu, Albert
57 APPLICANT: Herrmann, Rafael
58 APPLICANT: Wong, James
59 TITLE OF INVENTION: Defensin Polynucleotides and Methods of
60 FILE OF INVENTION: Use
61 FILE REFERENCE: 35718/246703
62 CURRENT APPLICATION NUMBER: US/10/178,213
63 CURRENT FILING DATE: 2002-06-21
64 PRIOR APPLICATION NUMBER: 60/300,152
65 PRIOR FILING DATE: 2001-06-22
66 PRIOR APPLICATION NUMBER: 60/300,241
67 PRIOR FILING DATE: 2001-06-22
68 NUMBER OF SEQ ID NOS: 469
69 SOFTWARE: FastSeq for Windows Version 4.0
70 SEQ ID NO: 469
71
72 SOFTWARE: FastSeq for Windows Version 4.0

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SEQ ID NO 439
LENGTH: 563
TYPE: DNA
ORGANISM: Cymopsis tetraginoloba
FEATURE:
NAME/KEY: CDS
LOCATION: (106)...(333)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (190)...(330)
US-10-178-213-439

Alignment Scores:
Pred. No.: 2,34e-18 Length: 563
Score: 183.00 Matches: 31
Percent Similarity: 87.50% Conservative: 4
Best Local Similarity: 77.50% Mismatches: 3
Query Match: 75.00% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-10-178-213-439 (1-563)

QY 2 ThrcyslunleuAlaasnThrTyArgGlyProCysPhe-----GlyGlyCysasp 19
|||||.....
DB 193 ACATGTAGAGTCTGGACACATACAGGGACCTGTTACACAGATGCTAGCTGCAT 252
|||||.....

QY 20 PheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39
|||||.....
DB 253 GATCAGCTGCAAGCAAGACAGCACTTAATCATGAGTGAAGATGACAAATGATTTTCGCTGT 312
|||||.....

RESULT 11
US-10-010-731-9
Sequence 9, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shan, Dilip Meganalal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-No. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MBOT-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one of (244, 305)
OTHER INFORMATION: /mod_base= OTHER
/note= "N" = A or C or G or T"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-010-731-9

Alignment Scores:
Pred. No.: 7.43e-17 Length: 327
Score: 171.00 Matches: 28
Percent Similarity: 86.11% Conservative: 3
Best Local Similarity: 77.78% Mismatches: 5
Query Match: 70.08% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-9 (1-327)

QY 4 GluAsnleuAlaasnThrTyArgGlyProCysPheGlyGlyCysAspPheHisCysLys 23
|||||.....
DB 1 GAGATTTGGCGGATAGATATAGGGACATGCTTAGTGTTGACACTCAGTGCACA 60
|||||.....

QY 24 ThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39
|||||.....
DB 61 ACCAAAGAGAACGACGATTAGTGAAGGTGTAGGATGATCTTTCGTTCT 108
|||||.....

RESULT 12
US-09-759-584-35
Sequence 35, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, ROBERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SFE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear

```
; MOLECULE TYPE: cDNA
US-09-759-584-35

Alignment Scores:
Pred. No.: 5.76e-16 Length: 141
Score: 162.00 Matches: 27
Percent Similarity: 77.50% Conservative: 4
Best Local Similarity: 67.50% Mismatches: 7
Query Match: 66.39% Indels: 2
DB: 10 Gaps: 1

US-10-010-731-14 (1-40) x US-09-759-584-35 (1-141)

OY 2 ThrcysgluasnleuAlaasnThrtyrArgglyProCysPhe-----GlyGlyCysasp 19
|||||
DB 4 ACTTGCAGAACCTTTCTGCACTTTCAGGACCATGCAATGCAATGCAACTGCAAC 63
|||||

OY 20 PheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39
|||||
DB 64 AAGCATGTGCAAGAACACAGACGACATCTTCTTCTGAGAGATGACAGATGATTCNNNTGC 123
|||||

RESULT 13
US-10-178-213-379
; Sequence 379, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178, 213
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 379
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Cyamopsis tetragonoloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(256)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (116)...(253)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2
; OTHER INFORMATION: n = A,T,C or G
US-10-178-213-379

Alignment Scores:
Pred. No.: 5.06e-12 Length: 464
Score: 140.00 Matches: 24
Percent Similarity: 80.00% Conservative: 4
Best Local Similarity: 68.57% Mismatches: 5
Query Match: 57.38% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-10-178-213-379 (1-464)

OY 2 ThrcysgluasnleuAlaasnThrtyrArgglyProCysPhe-----GlyGlyCysasp 19
|||||
```

```
DB 119 ACATGTGAGAGTCCGCGAGACACATACAGGGACCTGTTTCACTGAGGGTAGCTGGCAT 178
OY 20 PheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArg 34
|||||
DB 179 GATCATTTGCAGAACAGAACACACTTATATGAGTGAACATGCAAA 223
|||||

RESULT 14
US-10-178-213-100
; Sequence 100, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178, 213
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Tulipa fosteriana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)...(225)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (91)...(222)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 147, 366, 371, 392, 396, 398, 415, 432, 438, 447, 453, 455,
; LOCATION: 458
; OTHER INFORMATION: n = A,T,C or G
US-10-178-213-100

Alignment Scores:
Pred. No.: 0.00075 Length: 471
Score: 85.50 Matches: 17
Percent Similarity: 53.66% Conservative: 5
Best Local Similarity: 41.46% Mismatches: 16
Query Match: 35.04% Indels: 3
DB: 9 Gaps: 2

US-10-010-731-14 (1-40) x US-10-178-213-100 (1-471)

OY 1 AlathrcysgluasnleuAlaasnThrtyrArgglyProCysPhe-----GlyGlyCys 18.
|||||
DB 91 GCAGATTGCTACAGACCGGAGGAGTTACACGCGCCCTCTTAGTTGAGCGGAGTGC 150
|||||

OY 19 AspPheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArg 38
|||||
DB 151 GATACCTACCTGCAGACATTCAGAGCGGCTCTCAGAGAGGGTCTTGC---AGCGGCTTCAAG 207
|||||

OY 39 Cys 39
DB 208 TGC 210

RESULT 15
US-10-178-213-106
; Sequence 106, Application US/10178213
; Publication No. US20030041348A1
```

GENERAL INFORMATION:

: APPLICANT: Simmons, Carl R.
 : APPLICANT: Navarro Acevedo, Pedro A.
 : APPLICANT: Harvell, Leslie
 : APPLICANT: Cahoon, Rebecca
 : APPLICANT: McCutchen, Billy Fred
 : APPLICANT: Lu, Albert
 : APPLICANT: Herrmann, Rafael
 : APPLICANT: Wong, James
 : TITLE OF INVENTION: Defense, Polynucleotides and Methods of
 : TITLE OF INVENTION: Use
 : FILE REFERENCE: 35718/246703
 : CURRENT APPLICATION NUMBER: US/10/178,213
 : CURRENT FILING DATE: 2002-06-21
 : PRIOR APPLICATION NUMBER: 60/300,152
 : PRIOR FILING DATE: 2001-06-22
 : PRIOR APPLICATION NUMBER: 60/300,241
 : PRIOR FILING DATE: 2001-06-22
 : NUMBER OF SEQ ID NOS: 469
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 106
 : LENGTH: 441
 : TYPE: DNA
 : ORGANISM: Tulipa gesneriana
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (44) ... (253)
 : FEATURE:
 : NAME/KEY: mat_peptide
 : LOCATION: (119) ... (250)
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: 24, 270, 294, 423
 : OTHER INFORMATION: n = A,T,C or G
 US-10-178-213-106

Alignment Scores:

Pred. No.: 0.00387 Length: 441
 Score: 80.50 Matches: 17
 Percent Similarity: 51.22% Conservative: 4
 Best Local Similarity: 41.46% Mismatches: 17
 Query Match: 32.99% Indels: 3
 DB: 9 Gaps: 2

US-10-010-731-14 (1-40) x US-10-178-213-106 (1-441)

QY 1 AlathrcysgluasnlauAlaSnThrTyTargGlyProGcysphe-----GlyGlyCys 18
 Db 119 GCGGATTGCTACAGACCGAGGCGGCGGCTTGTGATTGCGACGCGCTGC 178
 QY 19 AspPhehiscyslysthrlysgluhisleuDeuSerglyArgCysArgAspdphearg 38
 Db 179 GATAGTACCTGCAAGATTTCAGAGCGGGAACCAAGAGGAGACTTGC---AGCGGCTTCCGC 235
 QY 39 Cys 39
 Db 236 TGC 238

Search completed: June 21, 2003, 09:04:37
 Job time : 97.8824 secs

Oy	2	Thrcysgluhsnleuilaantrhrryrragglvprocsphhegllylcysasphhehis	21
Dd	108	ACATGTCAGAAATTGGCAGCATTAATATTAAGGGACCATGCTTTAGTGGTTGTACACTAC	167
Oy	22	CysLysThrLysGluHisIleuSerGlyArgCysArgAspAspPheArgCys	39
Dd	168	TGCACAACCAAAAGAACGACGACTTACTGGAAGGTGAGGACGACTTCGCGTGC	221
RESULT 5			
AAV39186			
ID	AAV39186	standard; DNA: 490 BP.	
XX			
AC	AAV39186:		
XX			
DT	01-OCT-1998	(first entry)	
DE			
XX			
XX	Antifungal polypeptide AlfAfp1 encoding cDNA.		
KW	Antifungal polypeptide: alfalfa plant; Medicago: fungal resistance;		
KW	plant pathogenic fungus; AlfAfp1, AlfAfp2; ss.		
XX			
OS	Medicago sativa.		
XX			
XX	Key	Location/Qualifiers	
FT	CDS	75..293	
FT		/*tag- a	
FT		/transl_except=(pos:129..131, aa:Glu)	
FT	slg_peptide	/product="AlfAfp1 polypeptide"	
FT		75..135	
FT		/*tag- b	
FT	mat_peptide	156..290	
FT		/*tag- c	
PN	W09826083-A1.		
PD	18-JUN-1998.		
XX			
XX	11-DEC-1997:	97WO-US22662.	
PR	13-DEC-1996:	96US-0766355.	
XX			
PA	(MONS) MONSANTO CO.		
PI	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;		
DR	WPI: 1998-348537/30.		
DR	P-PSDB: AAM61967.		
XX			
XX			
PS	Claim 5; Fig 1: 97bp; English.		
XX			
CC	This cDNA encodes an antifungal polypeptide, AlfAfp1 isolated from		
CC	alfalfa plants (Medicago). The polypeptides AlfAfp1 and AlfAfp2 are		
CC	used to control plant fungi, especially pathogenic fungi, by		
CC	transforming plant cells with a vector comprising sequences encoding		
CC	AlfAfp1 or AlfAfp2 to allow expression of antifungally effective amounts		
CC	of the polypeptide. Such transformed plants may be e.g. apple, wheat,		
CC	cotton and especially potato. Micro-organisms may also be transformed		
CC	to produce the polypeptides, and applied to plants to control plant		
CC	fungi. The polypeptides can also be included with a suitable solvent in		
CC	antifungal compositions and these can be administered to plants to		
CC	control plant fungi. Such compositions and genetically engineered plants		
CC	may also contain additional molecules e.g. the compositions can contain		
CC	other antifungal agents or the plants contain DNA encoding insecticidal		
CC	(e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful		
CC	to prepare antibodies useful to detect polypeptides or isolate other		
CC	alfalfa plant antifungal protein antigens. The nucleic acids are useful		
CC	to produce polypeptides and transgenic plants and as probes or primers in		
CC	nucleic acid hybridisation e.g. to detect complementary sequences in		

CC	samples, and to prepare mutants or isolate similar sequences from related
CC	species.
XX	
SQ	Sequence 490 BP; 182 A; 85 C; 85 G; 136 T; 2 other;
	Alignment Scores:
	Pred. No.: 2,836-16
	Score: 185.00
	Percent Similarity: 86.84%
	Best Local Similarity: 78.95%
	Query Match: 75.82%
	DB: 19
	Gaps: 0
US-10-010-731-14	(1-40) x AAV39186 (1-490)
OY	2 ThrcysGluasnLueAlAasnThrrYrgrGlyProCysPheGlycYcysAspPheNis 21
DB	159 ACATGTGAGAAATTTTGCAGATTAATATATAGGGACCATGCTTTAGTGGTTGTGCACTGC 218
OY	22 CysLstYThrLysGluHisLeuLeuSerGlyArGcysArGAspAspPheArGcys 39
DB	219 TGCACACCAAAAGACAGCAGCATGTAGTGGAGGTGAGGACGACATCCGCTGC 272
RESULT 6	
AAV39195	
ID	AAV39195 standard; DNA: 507 BP.
XX	
AC	AAV39195;
XX	
DT	25-SEP-1998 (first entry)
XX	
DE	Antifungal polypeptide AlfaFP1 mature sequence encoding DNA.
XX	
KW	Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance;
KW	plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
XX	
OS	Medicago sativa.
XX	
XX	
EH	Key Location/Qualifiers
FT	CDS 173..310
FT	/tag= a
FT	/product= "mature AlfaFP1"
XX	
XX	
PN	W098626083-A1.
XX	
PD	18-JUN-1998.
XX	
PE	11-DEC-1997; 97WO-US22662.
XX	
PR	13-DEC-1996; 96US-0766355.
XX	
PA	(MONS) MONSANTO CO.
XX	
PI	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX	
DR	WPI; 1998-348537/30.
DR	P-PSDB; AAM61964.
XX	
PT	Antifungal poly(peptide)s and genes isolated from alfalfa plant(s)
PT	- used to control plant pathogenic fungi and to produce transformed
XX	
PS	plants with increased fungal resistance
XX	
XX	Claim 5; Page 77; 97pp; English.
CC	
CC	This DNA encodes an antifungal polypeptide, AlfaFP1 isolated from
CC	alfalfa plants (Medicago). The polypeptides AlfaFP1 and AlfaFP2 are
CC	useful to control plant fungi, especially pathogenic fungi, by
CC	transforming plant cells with a vector comprising sequences encoding
CC	AlfaFP1 or AlfaFP2 to allow expression of antifungally effective amounts
CC	of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC	cotton and especially potato. Micro-organisms may also be transformed
CC	to produce the polypeptides, and applied to plants to control plant
CC	fungi. The polypeptides can also be included with a suitable solvent in

CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. *Bacillus thuringiensis*) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 507 BP, 181 A, 85 C, 102 G, 136 T, 3 other;

Alignment Scores:
Pred. No.: 2,96e-16 Length: 507
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 19 Gaps: 0

US-10-010-731-14 (1-40) x AAV39195 (1-507)

OY 2 ThrcysgluasnlleualaasnthrttYtargglyProCyspHeGlyGlyCysAspPheHis 21
DB 176 ACATGTGAGATTTGGCAGATAAATATAGGGACCATGCTTTAGCTGTGGACACTTCAC 235

OY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspPheArgCys 39
DB 236 TGCACACCAAGAGAACGACGATTAGTGAAGGTGTAGGAGCAGACTTCGCTGC 289

RESULT 7
AAZ49412
ID AAZ49412 standard; cDNA: 468 BP.
XX
AC AAZ49412;
XX
DT 04-APR-2000 (first entry)
XX
DE Pea Defensin protein Drr230, encoding cDNA.
XX
KW Transgenic plant; disease resistance: DRR206; defensin; Drr230; PR10.1;
KW chitinase; recombinant expression system; Pea; Canola; Blackleg fungus;
KW CamV 35S inducible promoter; T-DNA; bacterial/fungal pathogen;
KW Leptosphaeria maculans; Rhizoctonia solani; Sclerotinia sclerotiorum; ds.
XX
OS Pisum sativum.
XX
XX
FH Key Location/Qualifiers
FT CDS 78..296
FT /*tag= a
FT /product= "Pea Defensin protein, Drr230"
FT /note= "Confers resistance against fungal and bacterial
FT pathogens"
XX
XX
PD WO200001824-A2.
XX
PN 13-JAN-2000.
XX
PD 13-JAN-2000.
XX
PF 02-JUL-1999; 99WO-CA00608.
XX
PR 03-JUL-1998; 98CA-2242116.
PR 06-JUL-1998; 98US-0091751.
XX
XX
PA (UYMA-) UNIV MANITOBA.
XX
PI Fristensky B, Wang Y;
XX
XX WPI: 2000-126938/11.
XX P-PSDB; AAY44509.
XX
PT Recombinant expression system for expressing DRR206 or defensin, used

PT to produce pathogen resistant Brassica napus -
XX
XX
PS Claim 11; Fig 9; 39pp; English.
XX
CC The present sequence is the cDNA encoding defensin protein, derived from
CC the clone Drr230 of Pea. This sequence is strongly induced by bacterial
CC and fungal pathogens like, blackleg fungus. This gene is used in a
CC recombinant expression system, capable of transforming plants like,
CC Canola (Brassica napus), under the constitutive control of CamV 35S
CC inducible promoter, responsive to pathogen infections. T-DNA sequence is
CC also present, for integration of the expression system into the plant
CC genome. Transgenic plants expressing DRR206 and defensin protein,
CC inhibited fungal growth in-vitro and are resistant to pathogenic
CC infections of Rhizoctonia solani, Leptosphaeria maculans and Sclerotinia
CC sclerotiorum.
XX
SQ Sequence 468 BP, 153 A, 88 C, 84 G, 143 T, 0 other;

Alignment Scores:
Pred. No.: 4.61e-15 Length: 468
Score: 176.00 Matches: 28
Percent Similarity: 86.84% Conservative: 5
Best Local Similarity: 73.68% Mismatches: 5
Query Match: 72.13% Indels: 0
DB: 21 Gaps: 0

US-10-010-731-14 (1-40) x AAZ49412 (1-468)

OY 2 ThrcysgluasnlleualaasnthrttYtargglyProCyspHeGlyGlyCysAspPheHis 21
DB 162 ACATGTGAGATTTGGCAGTTCATATPAGGAGAGTATGCTTCGGGTGGACGCTTCAC 221

OY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspPheArgCys 39
DB 222 TGTAGACACCAAGAGGCGCAATTAGCGCGCAGATGACGAGTACCTTCGCTGT 275

RESULT 8
AAV39194
ID AAV39194 standard; DNA: 327 BP.
XX
AC AAV39194;
XX
DT 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfaFP2 3' region.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
XX
XX
OS Medicago sativa.
XX
OS
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DW, Wu YS;
XX
XX WPI: 1998-348537/30.
XX
XX
XX Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)
XX - used to control plant pathogenic fungi and to produce transformed
XX plants with increased fungal resistance
XX
XX Claim 18; Page 77; 97pp; English.
XX
XX This sequence represents the 3' region of the DNA encoding an antifungal
XX polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The

CC polypeptides AlfAP1 and AlfAP2 are useful to control plant fungi,
 CC especially pathogenic fungi, by transforming plant cells with a vector
 CC comprising sequences encoding AlfAP1 or AlfAP2 to allow expression of
 CC antifungal effective amounts of the polypeptide. Such transformed
 CC plants may be e.g. apple, wheat, cotton and especially potato.
 CC Micro-organisms may also be transformed to produce the polypeptides, and
 CC applied to plants to control plant fungi. The polypeptides can also be
 CC included with a suitable solvent in antifungal compositions and these can
 CC be administered to plants to control plant fungi. Such compositions and
 CC genetically engineered plants may also contain additional molecules e.g.
 CC the compositions can contain other antifungal agents or the plants
 CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)
 CC proteins. The polypeptides are also useful to prepare antibodies useful
 CC to detect polypeptides or isolate other alfalfa plant antifungal protein
 CC antigens. The nucleic acids are useful to produce polypeptides and
 CC transgenic plants and as probes or primers in nucleic acid hybridisation
 CC e.g. to detect complementary sequences in samples, and to prepare mutants
 CC or isolate similar sequences from related species.

XX Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other;

Alignment Scores:

Pred. No.:	142e-14	Length:	327
Score:	171.00	Matches:	28
Percent Similarity:	86.11%	Conservative:	3
Best Local Similarity:	77.78%	Mismatches:	5
Query Match:	70.08%	Indels:	0
DB:	19	Gaps:	0

US-10-010-731-14 (1-40) x AAV39194 (1-327)

OY 4 GluAsnLeuAlaAsnThrTyArgGlyProCysPheGlyGlyCysAspPheHisCysLys 23
 DB 1 GAGATATTGGGGGATAGATATAGGGACCATGCTTACTGTTGACACACACACACACA 60
 OY 24 ThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39
 DB 61 ACCAAGAGAAAGCAGATTAGTGAGAGGTGATGATGATGATGATGATGATGATGATGAT 108

RESULT 9

ID AAQ70126 standard; cDNA; 141 BP.

AC AAQ70126;

DT 14-FEB-1995 (first entry)

DE Antimicrobial Lc-AFP.

KW Antimicrobial; Lc-AFP; symbiosis; disease-resistance;

KW fungus-resistance; *Clavibacter xyli* subsp. *cynodontis*; Cxc;

KW crop improvement; endophyte; ss

OS *Lathyrus cicerca*.

XX WO9416076-A.

XX 21-JUL-1994.

XX 05-JAN-1994; 94WO-GB00012.

XX 08-JAN-1993; 93GB-0000281.

XX (ZENEC) ZENEC LTD.

XX Dubock AC, Powell KA, Rees SB;

XX WPI; 1994-249223/30.

XX P-PSDB; AAR57322.

PT Antimicrobial protein producing endo-symbiotic microorganisms -
 PT is produced by combining nucleic acids encoding the protein with
 PT an endophyte, useful for protecting plant hosts from esp. fungal

PT disease
 XX
 PS Disclosure; Page 30; 39pp; English.

CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC *Clavibacter xyli* subsp. *cynodontis* (Cxc). Plants or seeds treated
 CC with recombinant Cxc are protected against fungal disease. A
 CC suitable antimicrobial protein is Lc-AFP from *L. cicerca*. A
 CC possible predicted sequence for the Lc-AFP gene is given in AAQ70126.

XX Sequence 141 BP; 43 A; 30 C; 32 G; 33 T; 3 other;

Alignment Scores:

Pred. No.:	8.42e-14	Length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	7
Query Match:	66.39%	Indels:	2
DB:	15	Gaps:	1

US-10-010-731-14 (1-40) x AAQ70126 (1-141)

OY 2 ThrCysGluAsnLeuAlaAsnThrTyArgGlyProCysPhe-----GlyGlyCysasp 19
 DB 4 ACTTCGAGAACCTTCTGAACTTCAAGGACCATGATCCAGATGAACTGCAC 63
 OY 20 PheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39
 DB 64 AAGCATTCGAAGAACACACAGCATCTCTTCTGGAAGATGACAGATGATTCNNNTGC 123

RESULT 10

ID AAQ38648 standard; DNA; 138 BP.

AC AAQ38648;

DT 07-JUL-1993 (first entry)

DE Encodes antifungal protein Lc-AFP1.

KW *Raphanus sativus*; Brassica; Arabidopsis; *Calceol*; *Lathyrus*; *Clitoria*;

KW fungicide; bactericide; antibiotic; antifungal; gram positive;

KW plant disease resistance; low toxicity.

OS *Lathyrus cicerca*.

XX Key Location/Qualifiers

FT CDS 1..138

FT /*tag= a

XX WO9305153-A.

XX 18-MAR-1993.

XX 27-AUG-1992; 92WO-GB01570.

XX 29-AUG-1991; 91GB-0018523.

XX 13-FEB-1992; 92GB-0003038.

XX 25-JUN-1992; 92GB-0013526.

XX (ICIL) IMPERIAL CHEM IND PLC.

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;

XX Vanderleyden J;

XX WPI; 1993-100978/12.

XX Biochemical proteins isolated from seeds of plants - e.g. brassica
 XX or dahlia, useful for increasing plants' resistance to fungal and
 XX bacterial diseases
 XX Disclosure; Fig 31A; 110pp; English.

CC PKM zeta inhibitor is useful for treating an animal suffering from
CC traumatic stress disorder, phobia, acute or chronic pain and epilepsy.
CC The method is also useful for treating drug or alcohol addiction and
CC in antisense therapy. The present sequence is human PKM zeta protein
CC encoding DNA.
XX

SO Sequence 2058 BP; 493 A; 572 C; 610 G; 381 T; 2 other;

Alignment Scores:

Pred. No.: 6,92 Length: 2058
Score: 71.50 Matches: 17
Percent Similarity: 51.288 Conservative: 3
Best Local Similarity: 43.598 Mismatches: 14
Query Match: 29.30% Indels: 5
DB: 24 Gaps: 2

US-10-010-731-14 (1-40) x AAF23627 (1-2058)

QY 3 CysGluAsnLeuAlaAsnThrTyrArgGlyProCysPheGlyGlyCysAspPheHisCys 22
DB 1892 TGTGCTGCTGCTCCGCGGATCCGCGGCGACCTGCGCGAGGGGCTGT-----CATGGC 1945
QY 23 LysThrLysGluHisLeuLeuSerGly-----ArgCysArgGspAspPheArg 38
DB 1946 GTTTCACAGGTGCACATTTCACACGGAACAGACTGATGACACTGCTCCGC 2002

RESULT 13

AAE21413 ID AAF21413 standard; DNA: 2146 BP.

XX AAF21413:

DT 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2980.

XX Low adenosine antisense oligonucleotide: phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
cancer; ss.

OS Homo sapiens.

PN MO200062736-A2.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000MO-US08020.

PR 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX NYCE JW;

DR WPI; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -

PS Disclosure; Page 1393-1394; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.

CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

SO Sequence 2146 BP; 506 A; 602 C; 633 G; 405 T; 0 other;

Alignment Scores:

Pred. No.: 7.3 Length: 2146
Score: 71.50 Matches: 17
Percent Similarity: 51.288 Conservative: 3
Best Local Similarity: 43.598 Mismatches: 14
Query Match: 29.30% Indels: 5
DB: 21 Gaps: 2

US-10-010-731-14 (1-40) x AAF21413 (1-2146)

QY 3 CysGluAsnLeuAlaAsnThrTyrArgGlyProCysPheGlyGlyCysAspPheHisCys 22
DB 1980 TGTGCTGCTGCTCCGCGGATCCGCGGCGACCTGCGCGAGGGGCTGT-----CATGGC 2033
QY 23 LysThrLysGluHisLeuLeuSerGly-----ArgCysArgGspAspPheArg 38
DB 2034 GTTTCACAGGTGCACATTTCACACGGAACAGACTGATGACACTGCTCCGC 2090

RESULT 14

AAA35291 ID AAA35291 standard; DNA: 2146 BP.

XX AAA35291:

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:165.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiallergic; cytostatic; analgesic; impeded airway;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN MO200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99MO-US17712.

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 05:44:53 ; Search time 1594.35 seconds

(without alignments)
730.147 Million cell updates/sec

Title: US-10-010-731-14

Perfect score: 244

Sequence: 1 ATCCENLANTYRGPCFCGCDPCKTKKHLKSGRCRDPFRC 40

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOR=ext -HEASize=500 -MINLEN=0 -MAXLEN=2000000000
-USFR=US10010731 @CGN.1.1.2566 @runat.17062003.095705.28161 -NCPU=6 -ICPU=3
-NO_MAMP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMOUT=120 -MARN_TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
1: gb_ba.*
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3: gb_in.*
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8: gb_pl.*
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10: gb_ro.*
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12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_ot.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*

29: em_vl.*
30: em_hlg_hum.*
31: em_hlg_inv.*
32: em_hlg_other.*
33: em_hlg_mus.*
34: em_hlg_pln.*
35: em_hlg_rtd.*
36: em_hlg_mem.*
37: em_hlg_vrt.*
38: em_sy.*
39: em_hlgo_hum.*
40: em_hlgo_mus.*
41: em_hlgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	194	79.5	436	AB020613	AB020613 Vigna rad
2	190	77.9	494	AX252303	AX252303 Sequence
3	185	75.8	406	AF319468	AF319468 Medicago
4	184	75.4	459	VUSTRORD	X16877 Vigna ungu
5	176	72.1	363	AF139018	AF139018 Pisum sat
6	176	72.1	468	PEADRR230A	LO1578 Pea (p1230)
7	176	72.1	468	PSPI230	X52225 P.sativum p
8	162	66.4	141	A27063	A27063 L.cicera AF
9	162	66.4	141	A39547	A39547 Sequence 35
10	162	66.4	141	AR050147	AR130266 Sequence
11	162	66.4	141	AR130266	123722 Sequence 35
12	162	66.4	141	I23722	I01579 Pisum sativ
13	131.5	53.9	456	PEADRR230B	X52224 P.sativum p
14	131.5	53.9	456	PSPI139	AB049718 Pisum sat
15	124	50.8	380	AB049718	AL732464 Mus muscu
16	124	32.2	200648	AL732464	BC014270 Homo sapi
17	124	29.7	2349	EC014270	AC120597 Homo sapi
18	124	29.7	130996	AC120597	AC112651 Homo sapi
19	124	29.7	159274	AC112651	AC084351 Homo sapi
20	124	29.7	171260	AC084351	U12150 Glycine max
21	124	29.3	527	GMU12150	AK097627 Homo sapi
22	124	29.3	1739	AK097627	AX286348 Sequence
23	124	29.3	2146	AX286348	AX333045 Sequence
24	124	29.3	2146	AX333045	Z15108 H.sapiens m
25	124	29.3	2216	HSPK2	AK055593 Homo sapi
26	124	29.3	2216	BC008058	BC008058 Homo sapi
27	124	29.3	2216	AL158042	AL158042 Human DNA
28	124	29.3	83777	AL158042	AL1590822 Homo sapi
29	124	29.3	178604	AC068198	AC068198 Homo sapi
30	124	29.3	213432	AC068198	AC095562 Rattus no
31	124	28.5	217775	AL592224	AL592224 Mouse DNA
32	124	28.5	217775	AC093839	AC093839 Homo sapi
33	124	28.3	162522	AC093839	AC093925 Genomic S
34	124	28.3	227242	AC093925	AC114617 Mus muscu
35	124	27.9	67994	AX046767	AX046767 Sequence
36	124	27.7	499	AX046767	AX046769 Sequence
37	124	27.7	517	AX046769	X16069 C.elegans h
38	124	27.7	13692	CELI107	AC006266 Arabidops
39	124	27.7	40970	CELI107	AC106180 Rattus no
40	124	27.7	105680	AC106180	AC113802 Rattus no
41	124	27.7	131586	AC113802	AC103190 Rattus no
42	124	27.7	159677	AC103190	AL161509 Arabidops
43	124	27.7	178989	ATCHRIV21	AC026076 Homo sapi
44	124	27.7	195837	AC026076	
45	124	27.5	214419	AC026076	

RESULT 1

ALIGNMENTS

AB020613
LOCUS AB020613 496 bp mRNA linear PLN 05-JAN-2002
DEFINITION Vigna radiata mRNA for PDF1, complete cds.
ACCESSION AB020613
VERSION AB020613.1 GI:18146787
KEYWORDS PDF1.
SOURCE Vigna radiata (strain:B20F5 9-3-2-2) Immature seed cDNA to mRNA,
clone_lib:B20 clone:pdf-1.
ORGANISM Vigna radiata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.
REFERENCE
1 Ishimoto, M. and Kaga, A.
Munbean defensin
JOURNAL Published only in Database (2002)
REFERENCE 2 (bases 1 to 496)
AUTHORS Ishimoto, M. and Kaga, A.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National
Agricultural Experiment Station, Laboratory of Plant Biotechnology;
6-12-1 Nishifukatsu, Fukuyama, Hiroshima 721-8514, Japan
(E-mail:ishimotoecgk@affrc.go.jp, Tel:+81-849-234100(ex.231),
Fax:+81-849-247893)
FEATURES
source
1. 496
/organism="Vigna radiata"
/strain="B20F5 9-3-2-2"
/db_xref="taxon:157791"
/clone="pdf-1"
/tissue_type="Immature seed"
/clone_lib="B20"
1. 496
/gene="PDF1"
46..273
/gene="PDF1"
/product="PDF1"
/codon_start=1
/protein_id="BAB82453.1"
/db_xref="GI:18146788"
/translation="MEKSLAGLCFLVLFVAQEVWVTEAKTCENLANTYRGPCFT
TSCDDHCNKEHLRSGRCRDPFCWCTRNC"
496
/gene="PDF1"
/note="17 a nucleotides"
BASE COUNT 148 a 104 c 106 g 138 t
ORIGIN
Alignment Scores:
Pred. No.: 2.07e-17 Length: 496
Score: 194.00 Matches: 34
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 4
Query Match: 79.51% Indels: 2
Gaps: 1
US-10-010-731-14 (1-40) x AB020613 (1-496)
QY 2 ThcCysGluAsnLeuAlaasnThrTYrArgGlyProCysPhe-----GlyGlyCysasp 19
|||||
Db 133 ACTTGGAGAACCTGGCGAATACTTACAGGGGTCATGCTTCACCACTGGCAGCTGCAT 192
20 PheHisCysLysThrIysGluHisLeuSerGlyArgCysArgAspPheArgCys 39
|||||
Db 193 GATCACTGCACAAGACAAGACACTTGAGGAGTGGCAGGTGCAGGACGATTTCCGGTGT 252
RESULT 2
LOCUS AX252303 494 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 5 from Patent WO0168887.
ACCESSION AX252303
VERSION AX252303.1 GI:15985643

KEYWORDS
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 494)
AUTHORS Jung, R. and Kinney, A.J.
TITLE Hypoallergenic transgenic soybeans
JOURNAL Patent: WO 0168887-A 5 20-SEP-2001;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
1. 494
/organism="Glycine max"
/db_xref="taxon:3847"
BASE COUNT 153 a 97 c 103 g 134 t 7 others
ORIGIN
Alignment Scores:
Pred. No.: 7.26e-17 Length: 494
Score: 190.00 Matches: 33
Percent Similarity: 85.00% Conservative: 1
Best Local Similarity: 82.50% Mismatches: 4
Query Match: 77.87% Indels: 2
Gaps: 1
US-10-010-731-14 (1-40) x AX252303 (1-494)
QY 2 ThcCysGluAsnLeuAlaasnThrTYrArgGlyProCysPhe-----GlyGlyCysasp 19
|||||
Db 133 ACTTGGAGAACCTGGCGTATACATPACAGGGGTCATGCTTCACCACTGGCAGCTGCAT 192
20 PheHisCysLysThrIysGluHisLeuSerGlyArgCysArgAspPheArgCys 39
|||||
Db 193 GATCACTGCACAAGACAAGACACTTGCTCAGAGGACGATGCGAGGACGATTTCCCTGT 252
RESULT 3
LOCUS AF319468 406 bp mRNA linear PLN 14-DEC-2000
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.
ACCESSION AF319468
VERSION AF319468.1 GI:11762085
KEYWORDS
SOURCE Medicago sativa.
ORGANISM Medicago sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 406)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., Rosenberger, C.A. and Hakimi, S.
TITLE Antifungal Polypeptide(s) and Methods for Controlling Plant
Pathogenic Fungi
JOURNAL Patent: US 6121436 19-SEP-2000;
Monsanto Company; St Louis, MO
2 (bases 1 to 406)
AUTHORS Gao, A.G., Hakimi, S.M., Mittanck, C.A., Wu, Y., Woerner, B.M.,
Starr, D.M., Shah, D.M., Liang, J. and Rommens, C.M.
TITLE Fungal pathogen protection in potato by expression of a plant
defensin peptide
JOURNAL Nat. Biotechnol. 18 (12), 1307-1310 (2000).
MEDLINE 20553844
PUBMED 11101813
REFERENCE
3 (bases 1 to 406)
AUTHORS Mittanck, C.A., Wu, Y., Hakimi, S.M., Liang, J., Shah, D.M. and Gao, A.G.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway,
St Louis, MO 63199, USA
FEATURES
source
1. 406
/organism="Medicago sativa"

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CDS
/db_xref="taxon:3879"
75..293
/note="alfAFP, defensin"
/codon_start=1
/product="antifungal protein precursor"
/protein_id="AAG40321.1"
/db_xref="GI:11762086"
/translation="MEKSLAGLCFLFLVFLVAQEIYVTEARTCEINLADKRGCFSG
CDHCTTKRENNVSGRCRDRFCWCTKRC"
75..155
/mat_peptide
156..290
/product="antifungal protein"
BASE COUNT 140 a 74 c 78 g 114 t
ORIGIN

Alignment Scores:
Pred. No.: 2.85e-16 Length: 406
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conserved: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
Gaps: 0

US-10-010-731-14 (1-40) x AF319468 (1-406)

Oy 2 ThrcysgluasnleuAlaasnThrTyrArgGlyProCysPheGlyGlyCysAspPheHis 21
Db 159 ACATGTGAGATTGGCGAGTAATATATAGGCGGACCATGCTTAACTGCTTGACACATCCAC 218
Oy 22 CysLysThrLysGluHisLeuLeuSerClyArgCysArgAspAspPheArgCys 39
Db 219 TGCACACCAAGAGAACGCAGTTAGTGGAAGGTGTAGGACGACCTTCGCTGC 272

RESULT 4
VUSTORED VUSTORED 459 bp mRNA linear PLN 12-SEP-1993
LOCUS Vigna unguiculata cDNA for stored cotyledon mRNA.
DEFINITION X16877
ACCESSION X16877.1 GI:22075
VERSION
KEYWORDS
SOURCE
ORGANISM
Vigna radiata.
Vigna radiata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.
1 (bases 1 to 459)
Yamauchi, D.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo
Metropolitan University, Fukuazawa 2-1, Setagaya-ku, Tokyo 158,
Japan
2 (bases 1 to 459)
Ishibashi, N., Yamauchi, D. and Minamikawa, T.
REFERENCE Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide
sequence of cloned cDNA for a stored mRNA and induction of its
synthesis by precocious germination
JOURNAL Plant Mol. Biol. 15 (1), 59-64 (1990)
MEDLINE 91355865
PUBMED 2103443
FEATURES
Source
Location/Qualifiers
1..459
/organism="Vigna radiata"
/db_xref="taxon:157791"
/clone="PSAS10"
/tissue_type="cotyledon"
/clone_lib="lambda gcl10"
/dev_stage="seed"
14..241
/note="PSAS10 ORF"
/codon_start=1
/protein_id="CAA34760.1"
/db_xref="GI:22076"

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BASE COUNT		136 a	91 c	99 g	133 t
ORIGIN		TGSCDDHCNKNEHLISGRCDVRCWCTRC"			
Alignment Scores:					
Pred. No.:	4.43e-16	Length:	459		
Score:	184.00	Matches:	32		
Percent Similarity:	82.50%	Conservative:	1		
Best Local Similarity:	80.00%	Mismatches:	5		
Query Match:	75.41%	Indels:	2		
DB:	8	Gaps:	1		
US-10-010-731-14 (1-40) x VUSTORED (1-459)					
Qy	2	ThrcysgiuAsnLeuAlaSnThrTyrArgGlyProCysPhe-----GlyGlyCysAsp	19		
Db	101	ACTTCGGAAACCTGGTGGATACATACAGGGGTCGGTCTTCACACCTGGAGCTGGCAT	160		
Qy	20	PheHiscysLysTrhTrhLysGluHisLeuDeuSerGlyArgCysArgAspSPheArGcys	39		
Db	161	GATCAGCTCAGAGACAAGACACACTGCTGTGAGTGGACAGCTCAGGATGATGCTCGGTGT	220		
RESULT 5					
LOCUS	AF139018	363 bp	mRNA	linear	PLN 02-JAN-2001
DEFINITION	Pisum sativum disease resistance response protein 230 precursor				
ACCESSION	AF139018				
VERSION	AF139018.1	GI:12002298			
KEYWORDS	Pisum sativum.				
SOURCE	Pisum sativum.				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.				
REFERENCE	1 (bases 1 to 363)				
AUTHORS	Savenstrand,H., Brosche,M. and Strid,A.				
TITLE	Stress-induced disease resistance response protein 230 cDNA from Pisum sativum cv. Greenfeast				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 363)				
AUTHORS	Savenstrand,H., Brosche,M. and Strid,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530, Sweden				
FEATURES					
source	Location/Qualifiers				
gene	1..363				
CDS	/organism="Pisum sativum"				
	/cultivar="Greenfeast"				
	/db_xref="taxon:3888"				
	1..363				
	/gene="DRR230"				
	56..274				
	/gene="DRR230"				
	/note="Ozone-induced, similar to the Pisum sativum cv. Alaska product encoded by Genbank Accession Number L01578"				
	/codon_start=1				
	/product="disease resistance response protein 230 precursor"				
	/protein_id="AA033285.1"				
	/db_xref="GI:12002298"				
	/translation="MEKKSILACSLFLLLVLEFAOEIVSEANTCENLAGSYKGVFGGGCDRHCRTOEGNISRCRCDPFCWCCTKNC"				
BASE COUNT	113 a	68 c	74 g	108 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	4.29e-15	Length:	363		
Score:	176.00	Matches:	28		

Percent Similarity: 86.84%
Best Local Similarity: 73.68%
Query Match: 72.13%
DB: 8
Conservative: 5
Matches: 5
Indels: 0
Gaps: 0

US-10-010-731-14 (1-40) x AF139018 (1-363)

QY 2 ThcysgluasnleuAlaasnThrTYrArgGlyProCysPheGlyCysAspPheHis 21
|||||
DB 140 ACATGTGAGAAATTGGCTGTCATATTAAGGAGATGCTTCGGTGGATGTGACCGTCAC 159
|||||

QY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39
|||||
DB 200 TGTAGAACAACAGAGCGCCGCAATTAGCGGAGATGAGGATGACTTCCCTGT 253
|||||

RESULT 6
PEADRR230A 468 bp mRNA linear PLN 11-FEB-2002
LOCUS
DEFINITION pea (p1230) disease resistance response protein 230 (DRR230-a)
ACCESSION
VERSION L01578.1 GI:169073
KEYWORDS cysteine-rich protein; disease resistance response protein 230;
pathogenesis-related protein.
SOURCE
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
REFERENCE
AUTHORS Chiang,C.C. and Hadwiger,L.A.
TITLE The fusarium solani-induced expression of a pea gene family
JOURNAL encoding high cysteine content proteins
MEDLINE M01. Plant Microbe Interact. 4 (4), 324-331 (1991)
PUBMED 92190628
COMMENT On Feb 8, 2002 this sequence version replaced gi:247416.
FEATURES
location/Qualifiers
1. 468
/organism="Pisum sativum"
/strain="Alaska"
/db_xref="taxon:3888"
/tissue_type="pod tissue treated with Fusarium solani
conidia"
/dev_stage="immature"
1. 468
/gene="DRR230-a"
78..296
/gene="DRR230-a"
/function="unknown"
/standard_name="pathogenesis related protein"
/note="p1230"
/codon_start=1
/evidence="experimental"
/product="disease resistance response protein"
/protein_id="AA09117.1"
/db_xref="GI:169074"
/translation="MEKKSILACISFLLVLFVAQELIVSEANTNCENLASIKYGVCRGS
CDRHCTOGCAISGRCDPFCMCTKNC"
159..293
mat_peptide
/gene="DRR230-a"
/product="disease resistance response protein"
/function="unknown"
/note="determined by in vitro cleavage with microsomal
membranes"
/evidence="experimental"

BASE COUNT 153 a 88 c 84 g 143 t
ORIGIN

Alignment Scores:
Pred. No.: 5.6e-15 Length: 468
Score: 176.00 Matches: 28

Percent Similarity: 86.84%
Best Local Similarity: 73.68%
Query Match: 72.13%
DB: 8
Conservative: 5
Matches: 5
Indels: 0
Gaps: 0

US-10-010-731-14 (1-40) x PEADRR230A (1-468)

QY 2 ThcysgluasnleuAlaasnThrTYrArgGlyProCysPheGlyCysAspPheHis 21
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DB 162 ACATGTGAGAAATTGGCTGTCATATTAAGGAGATGCTTCGGTGGATGTGACCGTCAC 221
|||||

QY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39
|||||
DB 222 TGTAGAACAACAGAGCGCCGCAATTAGCGGAGATGAGGATGACTTCCCTGT 275
|||||

RESULT 7
PSP1230 468 bp mRNA linear PLN 09-AUG-2002
LOCUS
DEFINITION P.sativum p1230 mRNA.
ACCESSION
VERSION X52225.1 GI:22208748
KEYWORDS secreted protein.
SOURCE
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
REFERENCE
AUTHORS Chiang,C.C. and Hadwiger,L.A.
TITLE The fusarium solani-induced expression of a pea gene family
JOURNAL encoding high cysteine content proteins
MEDLINE M01. Plant Microbe Interact. 4 (4), 324-331 (1991)
PUBMED 92190628
COMMENT Direct Submission
AUTHORS Chiang,C.
TITLE Submitted (03-AUG-1990) Chiang C., Washington State University,
JOURNAL Dept. of Plant Pathology, Pullman, WA 99164-6430, USA
FEATURES
location/Qualifiers
1. 468
/organism="Pisum sativum"
/db_xref="taxon:3888"
/tissue_type="endocarp"
1. 468
/gene="p1230"
78..296
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/product="CA36474.1"
/protein_id="CA36474.1"
/db_xref="GI:22208749"
/translation="MEKKSILACISFLLVLFVAQELIVSEANTNCENLASIKYGVCRGS
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78..158
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159..293
mat_peptide
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/product="unnamed"

BASE COUNT 153 a 88 c 84 g 143 t
ORIGIN

Alignment Scores:
Pred. No.: 5.6e-15 Length: 468
Score: 176.00 Matches: 28
Percent Similarity: 86.84% Conservative: 5
Best Local Similarity: 73.68% Matches: 5
Query Match: 72.13% Indels: 0
DB: 8 Gaps: 0
US-10-010-731-14 (1-40) x PSP1230 (1-468)
QY 2 ThcysgluasnleuAlaasnThrTYrArgGlyProCysPheGlyCysAspPheHis 21
|||||

Df	162	ACATGTGGAATTGGCTTGTTTCATATPAAAGGAGATGCTTCCGGTGGATGTGACCGTCAC	221
Oy	22	CysLysThrIlyrSGluHisLeuLeuSerIlyArgCysAsgAspSPheArgCys	39
Df	222	TGTAGAACAACAAGAGGGCGCAATTAACGCCGAGATGCAGGATGACTTTCGCTGT	275
RESULT 8	AZ7063		
LOCUS	AZ7063	141 bp	DNA linear PAT 12-JUN-1995
DEFINITION	L.cicera AFP sequence.		
ACCESSION	AZ7063		
VERSION	AZ7063.1	GI:1247357	
KEYWORDS	.		
SOURCE	Lathyrus cicera.		
ORGANISM	Lathyrus cicera		
FEATURES	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Lathyrus.		
source	Location/Qualifiers 1..141 /organism="Lathyrus cicera" /db_xref="taxon:3856"		
BASE COUNT	43 a 30 c 32 g 33 t		3 others
ORIGIN			
Alignment Scores:			
Pred. No.:	1..31e-13	Length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	7
Query Match:	66.39%	Indels:	2
DB:	6	Gaps:	1
US-10-010-731-14 (1-40) x AZ7063 (1-141)			
Oy	2	ThrcysgluasnleuAlasnrThrrYArglyProCysPhe-----GlyGLYCysasp	19
Df	4	ACTTGCAGAACCTTTCTCGAACTTTCAGGGACCATCATTCACAGATGGAACCTGCAC	63
Oy	20	PheHisCysLystrHrlySGluHisLeuLeuSerIlyArgCysAsgAspSPheArgCys	39
Df	64	AAGCATTCAGACACACAGACAGACTCTTTCTCTGAGAGATGCACAGATGATTCNNNTGC	123
RESULT 9	A39547	141 bp	DNA linear PAT 05-MAR-1997
LOCUS	A39547		
DEFINITION	Sequence 35 from Patent W09416076.		
ACCESSION	A39547		
VERSION	A39547.1	GI:2295840	
KEYWORDS	.		
SOURCE	unidentified.		
ORGANISM	unidentified		
REFERENCE	unclassified.		
AUTHORS	1 (bases 1 to 141)		
TITLE	Dubock A.C., Powell K.A. and Rees S.B.		
JOURNAL	ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS		
COMMENT	Patent: WO 9416076-A 35 21-JUL-1994;		
FEATURES	ZENECA LTD (GB) Other publication AU 5820494 940815. Location/Qualifiers 1..141 /organism="unidentified" /db_xref="taxon:32644"		
BASE COUNT	43 a 30 c 32 g 33 t		3 others
ORIGIN			
Alignment Scores:			
Pred. No.:	1..31e-13	Length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	7
Query Match:	66.39%	Indels:	2

DB:	6	Gaps:	1
US-10-010-731-14 (1-40) x A39547 (1-141)			
Oy	2	ThrcysgluasnlleuAlaasnThrTyArgGlyProCysPhe-----GlyGlyCysasp	19
			11
			11
			11
			11
Db	4	ACTTGCAGAACCTTTCTGGAACTTTCAGGACCATTCACAGATGGAACATCGAAC	63
Oy	20	PheHiscysLysThrLysGlnHisLeuSerGlyArgCysArgAspPheArgCys	39
			11
			11
			11
Db	64	AAGCATTTGCAAGAACAGACCATCTTCTCTGGAAGATGCAGAGATGATTCNNNTGC	123
RESULT 10			
LOCUS	AR050147	141 bp	DNA
DEFINITION	Sequence 35 from patent US 5824869.		linear
ACCESSION	AR050147		
VERSION	AR050147.1		
KEYWORDS	GI:5972139		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 141).		
AUTHORS	Broekert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B., Terras,F.R.G. and Vanderleyden,J.		
TITLE	Biocidal proteins		
JOURNAL	Patent: US 5824869-A 35 20-OCT-1998;		
FEATURES	Location/Qualifiers		
source	1..141		
BASE COUNT	43 a 30 c 32 g	33 t-	3 others
ORIGIN	/organism="unknown"		
Alignment Scores:			
Pred. No.:	1,31e-13	length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	7
Query Match:	66.39%	Indels:	2
DB:	6	Gaps:	1
US-10-010-731-14 (1-40) x AR050147 (1-141)			
Oy	2	ThrcysgluasnlleuAlaasnThrTyArgGlyProCysPhe-----GlyGlyCysasp	19
			11
			11
			11
			11
Db	4	ACTTGCAGAACCTTTCTGGAACTTTCAGGACCATTCACAGATGGAACATCGAAC	63
Oy	20	PheHiscysLysThrLysGlnHisLeuSerGlyArgCysArgAspPheArgCys	39
			11
			11
			11
Db	64	AAGCATTTGCAAGAACAGACCATCTTCTCTGGAAGATGCAGAGATGATTCNNNTGC	123
RESULT 11			
LOCUS	AR130266	141 bp	DNA
DEFINITION	Sequence 35 from patent US 6187904.		linear
ACCESSION	AR130266		
VERSION	AR130266.1		
KEYWORDS	GI:14118163		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 141)		
AUTHORS	Broekert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B., Terras,F.R.G. and Vanderleyden,J.		
TITLE	Biocidal proteins		
JOURNAL	Patent: US 6187904-A 35 13-FEB-2001;		
FEATURES	Location/Qualifiers		
source	1..141		
BASE COUNT	43 a 30 c 32 g	33 t	3 others
ORIGIN	/organism="unknown"		
Alignment Scores:			

Pred. No.: 1,31e-13 Length: 141
Score: 162.00 Matches: 27
Percent Similarity: 77.50% Conservative: 4
Best Local Similarity: 67.50% Mismatches: 7
Query Match: 66.39% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-14 (1-40) x AR130266 (1-141)

QY 2 ThrCysGluAsnLeuAlaAsnThrTyrArgGlyProCysPhe-----GlyGlyCysAsp 19
|||||
4 ACTTGGAGAACCTTTCTGAGACTTTCAGAGCAGCATCTCCAGATGGAACTGCAC 63

QY 20 PheHisCysLysThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39
|||||
64 AACGATTGCAAGAACAGCAGCATCTTCTTCTGGAAGATGACAGATGATTCNNNTGC 123

RESULT 12
LOCUS 123722 141 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 35 from patent US 5538525.
ACCESSION 123722
VERSION 123722.1 GI:1603592
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 141)
Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biochemical proteins
Patent: US 5538525-A 35 23-JUL-1996;
Location/Qualifiers
1..141
/organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 1,31e-13 Length: 141
Score: 162.00 Matches: 27
Percent Similarity: 77.50% Conservative: 4
Best Local Similarity: 67.50% Mismatches: 7
Query Match: 66.39% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-14 (1-40) x I23722 (1-141)

QY 2 ThrCysGluAsnLeuAlaAsnThrTyrArgGlyProCysPhe-----GlyGlyCysAsp 19
|||||
4 ACTTGGAGAACCTTTCTGAGACTTTCAGAGCAGCATCTCCAGATGGAACTGCAC 63

QY 20 PheHisCysLysThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39
|||||
64 AACGATTGCAAGAACAGCAGCATCTTCTTCTGGAAGATGACAGATGATTCNNNTGC 123

RESULT 13
PEADRR230B 456 bp mRNA linear PLN 11-FEB-2002
LOCUS
DEFINITION Pisum sativum disease resistance response protein 39 (DRR230-B)
ACCESSION L01579.1 GI:169075
VERSION L01579.1 GI:169075
KEYWORDS cysteine-rich protein; disease resistance response protein 39;
pathogenesis-related protein.
SOURCE Pisum sativum (strain Alaska) CDNA to mRNA.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.
1 (bases 1 to 456)

REFERENCE 1
AUTHORS Chiang, C.C. and Hadwiger, L.A.

TITLE The Fusarium solani-induced expression of a pea gene family
encoding high cysteine content proteins
JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
MEDLINE 92190628
PUBMED 1799696
COMMENT On Feb 8, 2002 this sequence version replaced gi:247414.
FEATURES
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1..456
/organism="Pisum sativum"
/strain="Alaska"
/db_xref="taxon:3888"
/tissue_type="pod tissue treated with Fusarium solani
conidia."
/dev_stage="immature"
1..456
/gene="DRR230-b"
69..293
/gene="DRR230-b"
/function="unknown"
/standard_name="pathogenesis related protein"
/evidence="experimental"
/product="disease resistance response protein 39"
/protein_id="AA079118.1"
/db_xref="GI:169076"
/translation="MEKSLAALSFLLVLVFAOEIVVTANTCEHLADTYRGVCF
NASCDHCKNMKHLISGTCHDMKCFCTQNC"
153..290
/gene="DRR230-b"
/product="disease resistance response protein"
/function="unknown"
/standard_name="pathogenesis related protein"
/note="cysteine content determined by homology with p1230;
putative"

mat_peptide

BASE COUNT 155 a 81 c 79 g 141 t
ORIGIN

Alignment Scores:

Pred. No.: 6,5e-09 Length: 456
Score: 131.50 Matches: 24
Percent Similarity: 72.50% Conservative: 5
Best Local Similarity: 60.00% Mismatches: 8
Query Match: 53.89% Indels: 2
DB: 8 Gaps: 3

US-10-010-731-14 (1-40) x PEADRR230B (1-456)

QY 2 ThrCysGluAsnLeuAlaAsnThrTyrArgGlyProCysPhe-----GlyGlyCysAsp 19
|||||
156 ACTTGGAGAACCTTTCTGAGACTTTCAGAGCAGCATCTTCCAGATGCTAGCTGAT 215

QY 20 PheHisCysLysThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39
|||||
216 GATCACTGCAAGAACAGCAGCATTAATCAGTGGACGTCGCAT--GACTGGAATGT 272

RESULT 14
PSP139 456 bp mRNA linear PLN 09-AUG-2002
LOCUS
DEFINITION P. sativum P139 mRNA.
ACCESSION X52224
VERSION X52224.1 GI:22208744
KEYWORDS secreted protein.
SOURCE pea.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.
1

REFERENCE 1
AUTHORS Chiang, C.C. and Hadwiger, L.A.
TITLE The Fusarium solani-induced expression of a pea gene family
encoding high cysteine content proteins
JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)


```

MEDLINE      92190628
REFERENCE    2 (bases 1 to 456)
AUTHORS      Chiang C.
TITLE        Direct Submission
JOURNAL      Submitted (03-AUG-1990) Chiang C., Washington State University,
              Dept. of Plant Pathology, Pullman, WA 99164-6430, USA
FEATURES
  source      1..456
              /organism="Pisum sativum"
              /db_xref="taxon:3888"
              /tissue_type="endocarp"
  gene        1..456
              /gene="P139"
  CDS         69..293
              /gene="P139"
              /codon_start=1
              /protein_id="CAA36473.1"
              /db_xref="GI:22208745"
              /translation="MEKSLALSLFLLLVFAOEIVVTEANTCEHLADFYRGVCF
              NASCDHCKNKKAHLISGICHDKCFCTONC"
  sig_peptide 69..152
              /gene="P139"
  mat_peptide 153..290
              /gene="P139"
              /product="unnamed"
  BASE COUNT 155 a      81 c      79 g      141 t
  ORIGIN
Alignment Scores:
  Pred. No.: 6.5e-09      Length: 456
  Score: 131.50      Matches: 24
  Percent Similarity: 72.50%      Conservative: 5
  Best Local Similarity: 60.00%      Mismatches: 8
  Query Match: 53.89%      Indels: 3
              Gaps: 2
  DB: 8
  US-10-010-731-14 (1-40) x PSP139 (1-456)
  QY          2 ThrCGSGIAsnLeuAlaAspThrTyrArgGlyProCysPhe-----GlyGlyCysAsp 19
              |||
              |||
  DB          156 ACTGTGTGACATTGTGGCTGATCATPACAGGAGATGCTTACAGCAATGCTAGCTGTGAT 215
              |||
              |||
  QY          20 PheHISGlySThrLysGluHisLeuLeuSerGlyArgCysArgSpAspPheArgCys 39
              |||
              |||
  DB          216 GATCACTGCAGAACAAAGCGCAGCTTAACATGCGACCTGCCAT---GACTGGAATAT 272
              |||
              |||
RESULT 15
AB049718      380 bp      mRNA      linear      PLN 08-JUN-2001
AB049718/C    Pisum sativum ssa-8 mRNA for putative senescence-associated
LOCUS         protein, complete cds.
ACCESSION     AB049718
VERSION       AB049718.1 GI:13359440
KEYWORDS
SOURCE
  ORGANISM    Pisum sativum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
  Pisum.
  1 (sites)
  Parlasca,J.A.T., Sunaga,A., Miyazaki,T., Hisaka,H., Sonoda,M.,
  Nakagawa,H. and Sato,T.
  Cloning of cDNAs encoding senescence-associated genes, ACC synthase
  and ACC oxidase from stored snow pea pods (Pisum sativum L. var
  saccharatum) and their expression during pod storage
  Postharvest Biology and Technology 22, 239-247 (2001)
  2 (bases 1 to 380)
  Parlasca,J.A. and Sato,T.
  Direct Submission
  Submitted (06-OCT-2000) Takahide Sato, Chiba University, Faculty of
  Horticulture; 648 Matsudo, Matsudo, Chiba 271-8510, Japan

```

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FEATURES
  source      (E-mail:sato@mori.h.chiba-u.ac.jp, Tel:81-47-308-8863)
              Location/Qualifiers
  1..380
              /organism="Pisum sativum"
              /cultivar="Ichihara wase"
              /db_xref="taxon:3888"
              /tissue_type="pods"
              /dev_stage="immatured pods"
              /country="Japan: Chiba, Matsudo"
              /note="cDNAs isolated from a 5-day stored pod cDNA library
              by differential screening"
  gene        1..380
              /gene="ssa-8"
  CDS         98..370
              /gene="ssa-8"
              /codon_start=1
              /product="putative senescence-associated protein"
              /protein_id="BAB3416.1"
              /db_xref="GI:13359441"
              /translation="MDIEYTHNSOSRIQHTGANVLIHIFLHISPIFLHLSLR
              VGEHNIINSECHSENHPCTSHSYVCARCCSNVCCSYHLCMPVFI"
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  ORIGIN
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  Best Local Similarity: 61.76%      Mismatches: 8
  Query Match: 50.82%      Indels: 2
              Gaps: 1
  DB: 8
  US-10-010-731-14 (1-40) x AB049718 (1-380)
  QY          8 AsnThrTyrArgGlyProCysPhe-----GlyGlyCysAspPheHISGlySThrLys 25
              |||
              |||
  DB          368 AATTAACACTGGACATGATCCAGATGTGTAACATGCAGAACATTCGACAGAACAC 309
              |||
              |||
  QY          26 GluHISLeuLeuSerGlyArgCysArgSpAspPheArgCys 39
              |||
              |||
  DB          308 GAGCACATCACTGAGTGGAGGTGCAGGATGATTTTCGCTGC 267
              |||
              |||
Search completed: June 21, 2003, 07:19:21
Job time : 1598.35 secs

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OM protein - nucleic search, using frame_p1us_p2n model

Run on: June 21, 2003, 05:44:53 ; Search time 1793.65 Seconds
(without alignments)
730.147 Million cell updates/sec

Title: US-10-010-731-2

Perfect score: 275
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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36: em_hgt_mam:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgt_hum:*
40: em_hgt_mus:*
41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	275	100.0	406	8	AF319468
2	214	77.8	363	8	AF139018
3	214	77.8	468	8	PEADRR230A
4	214	77.8	468	8	PSPT230
5	206	74.9	494	6	AX252303
6	199	72.4	496	8	AB020613
7	197	71.6	459	8	VUSTORED
8	168	61.1	141	6	A27063
9	168	61.1	141	6	A39547
10	168	61.1	141	6	AR050147
11	168	61.1	141	6	ARI30266
12	168	61.1	141	6	I23722
13	141.5	51.5	456	8	PEADRR230B
14	141.5	51.5	456	8	PSPT39
15	141	51.3	380	8	AB049718
16	103	37.5	527	8	GMU12150
17	99	36.0	733	8	AF417297
18	95	34.5	612	8	AB034956
19	94	34.2	382	8	AB052687
20	93	33.8	439	8	AF141131
21	93	33.8	472	8	AF178634
22	92	33.5	469	8	LES133601
23	92	33.5	5461	8	CACRTHIOGN
24	91	33.1	265	8	AY079405
25	91	33.1	486	8	NTDEFENSI
26	91	33.1	515	8	AY050979
27	91	33.1	93212	8	AC005936
28	90	32.7	470	8	ST332R
29	90	32.7	1561	8	PETSTHIONI
30	88	32.0	526	8	AY087062
31	87	31.6	469	8	ATP11A
32	87	31.6	507	8	AF370355
33	86	31.3	481	8	BRRIIF25
34	85	30.9	403	8	OSU72942
35	85	30.9	1459	8	AF044059
36	85	30.9	154128	8	AP000615
37	83	29.8	2	2	AP004836
38	82	29.8	512	8	AF442388
39	82	29.8	2000	6	AX461158
40	81	29.5	490	8	PASPT1GEN
41	81	29.5	1370	4	AY039681
42	80.5	29.3	85355	2	AC019557
43	80.5	29.3	172284	3	AC010018
44	80.5	29.3	178019	3	AC091206
45	80.5	29.3	180859	2	AC091126

RESULT 1

ALIGNMENTS

AF139468
LOCUS AF139468 406 bp mRNA linear PLN 14-DEC-2000
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.
ACCESSION AF139468
VERSION AF139468.1 GI:11762085
KEYWORDS
SOURCE Medicago sativa
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
REFERENCE 1 (bases 1 to 406)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., Rosenberger, C.A. and Hakim, S.
TITLE Antifungal Polypeptide(s) and Methods for Controlling Plant Pathogenic Fungi
JOURNAL Patent: US 6121436 19-SEP-2000;
Monsanto Company; St Louis, MO
REFERENCE 2 (bases 1 to 406)
AUTHORS Gao, A.G., Hakim, S.M., Miltanck, C.A., Wu, Y., Woerner, B.M., Stark, D.M., Shah, D.M., Liang, J. and Rommens, C.M.
TITLE Fungal pathogen protection in potato by expression of a plant defense peptide
JOURNAL Nat. Biotechnol. 18 (12), 1307-1310 (2000)
MEDLINE 2053844
PUBMED 11101813
REFERENCE 3 (bases 1 to 406)
AUTHORS Miltanck, C.A., Wu, Y., Hakim, S.M., Liang, J., Shah, D.M. and Gao, A.G.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway, St Louis, MO 63198, USA
FEATURES
source 1. 406
/organism="Medicago sativa"
/db_xref="taxon:3879"
75..293
/note="alfap; defensin"
/codon_start=1
/product="antifungal protein precursor"
/protein_id="AAC40321.1"
/db_xref="GI:11762085"
/translation="MERKSLAGLCFLVLFVAQELIVTEARTICENLADKYKSPCTSG CDHCTTKENAVSGRCRDPFCWCTKRC"
sig_peptide
mat_peptide
BASE COUNT 140 a 74 c 78 g 114 t
ORIGIN
Alignment Scores:
Pred. No.: 3, 21e-23 Length: 406
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-010-731-2 (1-45) x AF139468 (1-406)
QY 1 ArgTThCysGluAsnLeuAlaAspLysTYrArgGLyProCysPheSerGLyCysAspThr 20
DB 156 AGAACATGTGAGATTGGCAGATTAATATAGGGGACCAATGCTTTAGTGGTTGTGACACT 215
QY 21 HlscYstThrThlySgluAsnAlaValSerGLyArgCysArgAspAspPheArgCysTTP 40
DB 216 CACTGCACAACCAAGAGAACCGACGTTAGTGAAGGTGTAGGAGCAGACTTCCGCTCTGG 275
QY 41 CystHlySargCys 45
DB 276 TGTACTAAAGATGT 290
RESULT 2
AF139018

LOCUS AF139018 363 bp mRNA linear PLN 02-JAN-2001
DEFINITION Pisum sativum disease resistance response protein 230 precursor (DRR230) mRNA, complete cds.
ACCESSION AF139018
VERSION AF139018.1 GI:12002298
KEYWORDS
SOURCE Pisum sativum
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
REFERENCE 1 (bases 1 to 363)
AUTHORS Sevenstrand, H., Brosche, M. and Strid, A.
TITLE Stress-induced disease resistance response protein 230 cDNA from Pisum sativum cv. Greenfeast
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 363)
AUTHORS Sevenstrand, H., Brosche, M. and Strid, A.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530, Sweden
FEATURES
source 1. 363
/organism="Pisum sativum"
/cultivar="Greenfeast"
/db_xref="taxon:3888"
1..363
/gene="DRR230"
56..274
/gene="DRR230"
/note="ozone-induced: similar to the Pisum sativum cv. Alaska product encoded by GenBank Accession Number L01578"
/codon_start=1
/product="disease resistance response protein 230 precursor"
/protein_id="AAC43285.1"
/db_xref="GI:12002299"
/translation="MERKSLAGLCFLVLFVAQELIVTEARTICENLADKYKSPCTSG CDHCTTKENAVSGRCRDPFCWCTKRC"
BASE COUNT 113 a 68 c 74 g 108 t
ORIGIN
Alignment Scores:
Pred. No.: 3, 38e-16 Length: 363
Score: 214.00 Matches: 33
Percent Similarity: 81.82% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 8
Query Match: 77.82% Indels: 0
DB: 8 Gaps: 0
US-10-010-731-2 (1-45) x AF139018 (1-363)
QY 2 ThnCysGluAsnLeuAlaAspLysTYrArgGLyProCysPheSerGLyCysAspThrHis 21
DB 140 ACATGTGAGAAATTGGCTGTCATATAGGAGATATGCTTCGGTGGATGTGACCTCAC 199
QY 22 CysTThrThlySgluAsnAlaValSerGLyArgCysArgAspAspPheArgCysTTPCys 41
DB 200 TGTAGAACACAMAGAGGCGCAATATACCGCAGATGACAGGATGACCTTTCGCTGTGTGC 259
QY 42 ThrLysArgCys 45
DB 260 ACTAAAACTGT 271
RESULT 3
PEADRR230A
LOCUS PEADRR230A 468 bp mRNA linear PLN 11-FEB-2002
DEFINITION pea (p1230) disease resistance response protein 230 (DRR230-a) mRNA, complete cds.
ACCESSION L01578.1
VERSION L01578.1 GI:169073

KEYWORDS
cysteine-rich protein; disease resistance response protein 230;
pathogenesis-related protein.

SOURCE
Pisum sativum.

ORGANISM
Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.

REFERENCE
1 (bases 1 to 468)
Chiang,C.C. and Hadwiger,L.A.
The Fusarium solani-induced expression of a pea gene family
encoding high cysteine content proteins

TITLE
Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)

JOURNAL
MEDLINE
92190628

PUBMED
1799696

COMMENT
On Feb 8, 2002 this sequence version replaced gi:247416.

FEATURES
source
1. 468
/organism="Pisum sativum"
/strain="Alaska"
/db_xref="taxon:3888"
/tissue_type="pod tissue treated with Fusarium solani
conidia"
/dev_stage="immature"
1. 468
/gene="DRR230-a"
78. 296
/gene="DRR230-a"
/function="unknown"
/standard_name="pathogenesis related protein"
/note="p1230"
/codon_start=1
/evidence="experimental"
/product="disease resistance response protein"
/protein_id="AAV9117.1"
/db_xref="GI:169074"
/translation="MEKSLACLSPFLLVFAOEIVSEANTCENLAGSKVCFGG
CDRHCRTOEGALISGRCDRDFRCWCTKNC"
159. 293
/gene="DRR230-a"
/product="disease resistance response protein"
/function="unknown"
/note="determined by in vitro cleavage with microsomal
membranes"
/evidence="experimental"

BASE COUNT
153 a 88 c 84 g 143 t

ORIGIN

Alignment Scores:
Pred. No.: 4.34e-16 Length: 468
Score: 214.00 Matches: 33
Percent Similarity: 81.82% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 8
Query Match: 77.82% Indels: 0
Gaps: 0

US-10-010-731-2 (1-45) x PEADRR230A (1-468)

QY 2 ThTCysGluAsnLeuAlaAspLysTYrArgGlyProCysPheSerGlyCysAspThrHis 21
|||||
Db 162 ACATGTGAGAAATTTCGCTGTCATTAAGGAGATGCTTCGCTGATGTGACCGGCAC 221
22 CysTThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTPCyS 41
||| |||
Db 222 TGTAGAACACAGAGGGCGCAATTAGCGGAGATGACGATCTTCCTGTTGGTGC 281
42 ThrLysArgCys 45
|||||
Db 282 ACTAAAAACTGT 293

RESULT 4
PSP1230 468 bp mRNA linear PLN 09-AUG-2002

DEFINITION
P.sativum p1230 mRNA.

ACCESSION
X52225

VERSION
X52225.1 GI:22208748

KEYWORDS
secreted protein.

SOURCE
Pisum sativum
Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.

REFERENCE
1
Chiang,C.C. and Hadwiger,L.A.
The Fusarium solani-induced expression of a pea gene family
encoding high cysteine content proteins

TITLE
Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)

JOURNAL
MEDLINE
92190628

REFERENCE
AUTHORS
Chiang,C.
Direct Submission
Submitted (03-AUG-1990) Chiang C., Washington State University,
Dept. of Plant Pathology, Pullman, WA 99164-6430, USA

FEATURES
source
1. 468
/organism="Pisum sativum"
/db_xref="taxon:3888"
/tissue_type="endocarp"
1. 468
/gene="p1230"
78. 296
/gene="p1230"
/function="unknown"
/codon_start=1
/protein_id="CAA36474.1"
/db_xref="GI:22208749"
/translation="MEKSLACLSPFLLVFAOEIVSEANTCENLAGSKVCFGG
CDRHCRTOEGALISGRCDRDFRCWCTKNC"
78. 158
/gene="p1230"
159. 293
/gene="p1230"
/product="unnamed"

BASE COUNT
153 a 88 c 84 g 143 t

ORIGIN

Alignment Scores:
Pred. No.: 4.34e-16 Length: 468
Score: 214.00 Matches: 33
Percent Similarity: 81.82% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 8
Query Match: 77.82% Indels: 0
Gaps: 0

US-10-010-731-2 (1-45) x PSP1230 (1-468)

QY 2 ThTCysGluAsnLeuAlaAspLysTYrArgGlyProCysPheSerGlyCysAspThrHis 21
|||||
Db 162 ACATGTGAGAAATTTCGCTGTCATTAAGGAGATGCTTCGCTGATGTGACCGGCAC 221
22 CysTThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTPCyS 41
||| |||
Db 222 TGTAGAACACAGAGGGCGCAATTAGCGGAGATGACGATCTTCCTGTTGGTGC 281
42 ThrLysArgCys 45
|||||
Db 282 ACTAAAAACTGT 293

RESULT 5
AX252303 494 bp DNA linear PAT 05-OCT-2001
LOCUS
DEFINITION
Sequence 5 from Patent WO0168887.
ACCESSION
AX252303.1 GI:15985643
VERSION
KEYWORDS
soybean.

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine

REFERENCE

1 (bases 1 to 494)
Jung, R. and Kinney, A. J.
Hypalllergenic transgenic soybeans
Patent: WO 0168887-A 5 20-SEP-2001;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)

FEATURES

Source
Location/Qualifiers
1..494
/organism="Glycine max"
/db_xref="taxon:3847"
BASE COUNT 153 a 97 c 103 g 134 t 7 others
ORIGIN

Alignment Scores:

Pred. No.: 3,87e-15 Length: 494
Score: 206.00 Matches: 33
Percent Similarity: 78.72% Conservative: 4
Best Local Similarity: 70.21% Mismatches: 8
Query Match: 74.91% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x AX252303 (1-494)

QY 1 ArgThrCysGluAsnAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18
:::|||||
DB 130 AACACTTGGCAGAACCTGGCTGATACATACAGGGGGTCCATGCTTCACACTGCACACTGC 189
QY 19 AspThrHisCysThrThrLysGluAsnAlaValSerClyArgCysArgAspAspPheArg 38
||| |||||
DB 190 GATGATCACCACGCAAGAACAAAGACACTTCTCAGAGGCGATGCGAGCGACGATTTCCG 249
QY 39 CysTrpCysThrLysArgCys 45
|||||
DB 250 TGTGGTGCGACCAAAACTGT 270

RESULT 6

AB020613 496 bp mRNA linear PLN 05-JAN-2002
LOCUS
DEFINITION Vigna radiata mRNA for PDF1, complete cds.
ACCESSION AB020613
VERSION AB020613.1 GI:18146787
KEYWORDS
SOURCE
Vigna radiata (strain:B20F5 9-3-2-2) immature seed cDNA to mRNA,
clone_lib:B20 clone:PDF-1.
Vigna radiata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.

REFERENCE

1
Ishimoto, M. and Kaga, A.
Mungbean defensin
Published only in Database (2002)
2 (bases 1 to 496)

AUTHORS

Ishimoto, M. and Kaga, A.

TITLE

JOURNAL

REFERENCE

Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National
Agricultural Experiment Station, Laboratory of Plant Biotechnology;
6-12-1 Nishifukatsu, Fukuyama, Hiroshima 721-8514, Japan
(E-mail:ishimoto@cgk.affrc.go.jp, Tel:+81-849-234100(ex.231),
Fax:+81-849-247893)

FEATURES

Source
Location/Qualifiers
1..496
/organism="Vigna radiata"
/strain="B20F5 9-3-2-2"
/db_xref="taxon:157791"
/clone="pdf-1"
/tissue_type="immature seed"

gene

CDS

/clone_lib="B20"
1..496
/gene="pdf1"
46..273
/gene="pdf1"
/codon_start=1
/product="pdf1"
/protein_id="BAB82453.1"
/db_xref="GI:18146788"
/translation="MERKSLAGICPLIVLFVAQVWVQTEAKTCENLANTYRPGCF
TGSCDDHCKKEHLRSGRCDPRCWRNC"
496
/gene="pdf1"
/note="17 a nucleotides"
polyA_site
BASE COUNT 148 a 104 c 106 g 138 t
ORIGIN

Alignment Scores:

Pred. No.: 2.52e-14 Length: 496
Score: 199.00 Matches: 32
Percent Similarity: 78.72% Conservative: 5
Best Local Similarity: 68.09% Mismatches: 8
Query Match: 72.36% Indels: 2
DB: 8 Gaps: 1

US-10-010-731-2 (1-45) x AB020613 (1-496)

QY 1 ArgThrCysGluAsnAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18
:::|||||
DB 130 AACACTTGGCAGAACCTGGCGAATACCTTACAGGGGGTCCATGCTTCACACTGCACACTGC 189
QY 19 AspThrHisCysThrThrLysGluAsnAlaValSerClyArgCysArgAspAspPheArg 38
||| |||||
DB 190 GATGATCACCACGCAAGAACAAAGACACTTAGAGAGTGGCGAGTGCAGGCGACGATTTCCG 249
QY 39 CysTrpCysThrLysArgCys 45
|||||
DB 250 TGTGGTGCGACTAGAAACTGT 270

RESULT 7

VUSTORED 459 bp mRNA linear PLN 12-SEP-1993
LOCUS
DEFINITION Vigna unguiculata cDNA for stored cotyledon mRNA.
ACCESSION X16877
VERSION X16877.1 GI:22075
KEYWORDS
SOURCE
Vigna radiata.
Vigna radiata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.

REFERENCE

1 (bases 1 to 459)
Yamauchi, D.
Direct Submission
Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo
Metropolitan University, Fukazawa 2-1, Setagaya-ku, Tokyo 158,
Japan

AUTHORS

TITLE

JOURNAL

REFERENCE

2 (bases 1 to 459)
Ishibashi, N., Yamauchi, D. and Minamikawa, T.
Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide
sequence of cloned cDNA for a stored mRNA and induction of its
synthesis by precocious germination
Plant Mol. Biol. 15 (1), 59-64 (1990)
JOURNAL MEDLINE 91355865
PUBMED 2103443

FEATURES

Source
Location/Qualifiers
1..459
/organism="Vigna radiata"
/db_xref="taxon:157791"
/clone="psAS10"
/tissue_type="cotyledon"
/clone_lib="lambda gt10"

CDS

/dev_stage="seed"
14..241
/note="PSAS10 ORF"
/codon_start=1
/protein_id="CA34760.1"
/db_xref="GI:22076"
/translation="MEKSIAGICFLFLVLFVAQEVVQSEAKTCENLVDTYRGPCFT
TGSCDHCNKKEHLISGRCDYRCWCTNC"

BASE COUNT 136 a 91 c 99 g 133 t

ORIGIN

Alignment Scores:
Pred. No.: 3,98e-14 Length: 459
Score: 197.00 Matches: 31
Percent Similarity: 76.60% Conservative: 5
Best Local Similarity: 65.96% Mismatches: 9
Query Match: 71.64% Indels: 2
DB: 8 Gaps: 1

US-10-010-731-2 (1-45) x VUSTORED (1-459)

OY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18
:::|||||
98 AAGACTGGCAGAACCTTGCTGATACAGGGGTCCTGCTTCACTGGAGCTGC 157

DB 158 GATGATCAGCTGCAGAACAGAACACTTGCTGATGAGGAGGATGATGTCGG 217

OY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
||| ||||| |||||
218 TGTGTGGTCACCGAACACTGT 238

DB 39 CysTrpCysThrLysArgCys 45
|||||
218 TGTGTGGTCACCGAACACTGT 238

RESULT 8

A27063 LOCUS A27063 141 bp DNA linear PAT 12-JUN-1995
DEFINITION L.cicera AFP sequence.
ACCESSION A27063
VERSION A27063.1 GI:1247357
KEYWORDS
SOURCE Lathyrus cicera.
ORGANISM Lathyrus cicera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaceae;
Lathyrus.
Location/Qualifiers
source 1..141
/organism="Lathyrus cicera"
/db_xref="taxon:3856"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

ORIGIN

Alignment Scores:
Pred. No.: 2,85e-11 Length: 141
Score: 168.00 Matches: 25
Percent Similarity: 70.21% Conservative: 8
Best Local Similarity: 53.19% Mismatches: 12
Query Match: 61.09% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x A27063 (1-141)

OY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18
:::|||||
1 AAGACTGGCAGAACCTTGCTGATGAGGAGCAGATTCAGATGGAACCTGC 60

DB 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
::: ||||| |||||
61 AACAGCATTTGCAGAACAGAGACATCTTCTTGAGAGATGACAGATGATTCNNN 120

OY 61 AACAGCATTTGCAGAACAGAGACATCTTCTTGAGAGATGACAGATGATTCNNN 120

DB 39 CysTrpCysThrLysArgCys 45

DB 121 TGCTGTGCACCTAGAACTGC 141

RESULT 9

A39547 LOCUS A39547 141 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 35 from Patent WO9416076.
ACCESSION A39547
VERSION A39547.1 GI:2295840
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 141)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 35 21-JUL-1994;
ZENECA LTD (GB)
COMMENT Other publication AU 5820494 940815.
FEATURES
source Location/Qualifiers
1..141
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

ORIGIN

Alignment Scores:
Pred. No.: 2,85e-11 Length: 141
Score: 168.00 Matches: 25
Percent Similarity: 70.21% Conservative: 8
Best Local Similarity: 53.19% Mismatches: 12
Query Match: 61.09% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x A39547 (1-141)

OY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18
:::|||||
1 AAGACTGGCAGAACCTTGCTGATGAGGAGCAGATTCAGATGGAACCTGC 60

DB 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
::: ||||| |||||
61 AACAGCATTTGCAGAACAGAGACATCTTCTTGAGAGATGACAGATGATTCNNN 120

OY 39 CysTrpCysThrLysArgCys 45
|||||
121 TGCTGTGCACCTAGAACTGC 141

RESULT 10

AR050147 LOCUS AR050147 141 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 35 from patent US 5824869.
ACCESSION AR050147
VERSION AR050147.1 GI:5972139
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 141)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Bioicidal proteins
JOURNAL Patent: US 5824869-A 35 20-OCT-1998;
FEATURES
source Location/Qualifiers
1..141
/organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

ORIGIN

Alignment Scores:
Pred. No.: 2,85e-11 Length: 141
Score: 168.00 Matches: 25
Percent Similarity: 70.21% Conservative: 8

Best Local Similarity: 53.19% Mismatches: 12
Query Match: 61.09% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x AR050147 (1-141)

QY 1 ArgThrcysgluasnleuAlaaspLysTYrArgGlyProCysphe-----SerGlyCys 18
1 AAGACTTGGCAGAACCTTCTTGCAGGACCATTCAGATGGAACCTGC 60
Db 19 AsptHthiscysThrThrLysgluasnAlaValSerGlyArgCysArgaspAspPheArg 38
61 AACAGCATTGCAAGAACCAAGACATCTTCTTGGAGATGCAGAGATGATTTCNNN 120

QY 39 CysTrpCysThrLysArgCys 45
121 TGCTGTGTCACCTAGAAACTGC 141
Db

RESULT 11
ARI30266 141 bp DNA Linear PAT 16-MAY-2001
LOCUS Sequence 35 from patent US 6187904.
DEFINITION ARI30266
ACCESSION ARI30266
VERSION ARI30266.1 GI:14118163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 141)
Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE
JOURNAL
FEATURES
source

Patent: US 6187904-A 35 13-FEB-2001;
Location/Qualifiers

1..141
/organism="unknown"
BASE COUNT 43 a 30 c 32 g 33 t 3 others

ORIGIN

Alignment Scores:
Pred. No.: 2.85e-11 Length: 141
Score: 168.00 Matches: 25
Percent Similarity: 70.21% Conservative: 8
Best Local Similarity: 53.19% Mismatches: 12
Query Match: 61.09% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x ARI30266 (1-141)

QY 1 ArgThrcysgluasnleuAlaaspLysTYrArgGlyProCysphe-----SerGlyCys 18
1 AAGACTTGGCAGAACCTTCTTGCAGGACCATTCAGATGGAACCTGC 60
Db 19 AsptHthiscysThrThrLysgluasnAlaValSerGlyArgCysArgaspAspPheArg 38
61 AACAGCATTGCAAGAACCAAGACATCTTCTTGGAGATGCAGAGATGATTTCNNN 120

QY 39 CysTrpCysThrLysArgCys 45
121 TGCTGTGTCACCTAGAAACTGC 141
Db

RESULT 12
123722 141 bp DNA Linear PAT 07-OCT-1996
LOCUS Sequence 35 from patent US 5538525.
DEFINITION 123722
ACCESSION 123722
VERSION 123722.1 GI:1603592
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 141)
Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,

Terras,F.R.G. and Vanderleyden,J.
TITLE
JOURNAL
FEATURES
source

Patent: US 5538525-A 35 23-JUL-1996;
Location/Qualifiers

1..141
/organism="unknown"
BASE COUNT 43 a 30 c 32 g 33 t 3 others

Alignment Scores:
Pred. No.: 2.85e-11 Length: 141
Score: 168.00 Matches: 25
Percent Similarity: 70.21% Conservative: 8
Best Local Similarity: 53.19% Mismatches: 12
Query Match: 61.09% Indels: 2
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x 123722 (1-141)

QY 1 ArgThrcysgluasnleuAlaaspLysTYrArgGlyProCysphe-----SerGlyCys 18
1 AAGACTTGGCAGAACCTTCTTGCAGGACCATTCAGATGGAACCTGC 60
Db 19 AsptHthiscysThrThrLysgluasnAlaValSerGlyArgCysArgaspAspPheArg 38
61 AACAGCATTGCAAGAACCAAGACATCTTCTTGGAGATGCAGAGATGATTTCNNN 120

QY 39 CysTrpCysThrLysArgCys 45
121 TGCTGTGTCACCTAGAAACTGC 141
Db

RESULT 13
PEARRR230B 456 bp mRNA Linear PLN 11-FEB-2002
LOCUS PEARRR230B
DEFINITION PEARRR230B
ACCESSION L01579.1 GI:169075
VERSION L01579.1 S88682
KEYWORDS cysteine-rich protein; disease resistance response protein 39;
pathogenesis-related protein.
SOURCE Pisinum sativum (strain Alaska) cDNA to mRNA.
ORGANISM Pisinum sativum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosoids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.

1 (bases 1 to 456)
Chiang,C.C. and Hadwiger,L.A.
The Fusarium solani-induced expression of a pea gene family
encoding high cysteine content proteins
Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
JOURNAL MEDLINE
PUBMED 92190628
COMMENT On Feb 8, 2002 this sequence version replaced gi:247414.
FEATURES

source

1..456
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/strain="Alaska"
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1..456
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69..293
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BASE COUNT          155 a      81 c      79 g      141 t

ORIGIN

Alignment Scores:

Pred. No.:          1.07e-07
Score:              141.50
Percent Similarity: 52.57%
Best Local Similarity: 59.17%
Query Match:        51.45%

DB:                 8
                    Gaps: 2

US-10-010-731-2 (1-45) x PSP139 (1-456)

QY 2 ThTCysGLuAsnLeuAlaAspLysTYrArgGlyProCysphe-----SerGlyCysAsp 19
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D156 ACTGTGAGCATTTGGCTGATACATACACAGGAGGAGTACGCTTCACGAATGCTAGCTGAT 215
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QY 20 ThHisCysThrTrpLysGLuAsnAlaValSerLysArgCysArgAspAspSphargCys 39
    |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
D216 GATCAGTCGCAAGAAAGCGCCACTTATACATGACGTGCACGTGCAT--GACTGGAATATGT 272
    |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|

QY 40 TrpCysThrLysArgCys 45
    ::|||.....|.....|.....|.....|.....|.....|.....|.....|.....|
D273 TTCTGCACCTCAAAACTGT 290

RESULT 15
AB049718/c          380 bp      mRNA      linear      PLN 08-JUN-2001
LOCUS              Pismu sativum ssa-8 mRNA for putative senescence-associated
DEFINITION         protein, complete cds.
ACCESSION          AB049718
VERSION            AB049718.1 GI:13359440
KEYWORDS

SOURCE

ORGANISM            Pismu sativum
                    Pismu sativum
                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                    Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
                    Pismu.
                    1 (sites)
                    Pariasca,J.A.T., Sunaga,A., Miyazaki,T., Hisaka,H., Sonoda,M.,
                    Nakagawa,H. and Sato,T.
                    Cloning of cDNAs encoding senescence-associated genes, ACC synthase
                    and ACC oxidase from stored snow pea pods (Pismu sativum L. var
                    saccharatum) and their expression during pod storage
                    Postharvest Biology and Technology 22, 239-247 (2001)
                    2 (bases 1 to 380)
                    Pariasca,J.A. and Sato,T.
                    Direct Submission
                    Submitted (06-OCT-2000) Takahide Sato, Chiba University, Faculty of
                    Horticulture, 648 Matsudo, Matsudo, Chiba 271-8510, Japan
                    (E-mail:sato@mdori.h.chiba-u.ac.jp, Tel:81-47-308-8863)

FEATURES
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                /cultivar="Ichihara wase"
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BASE COUNT 120 a 78 c 64 g 118 t
ORIGIN

Alignment Scores:
Pred. No.: 1.02e-07 Length: 380
Score: 141.00 Matches: 22
Percent Similarity: 67.50% Conservative: 5
Best Local Similarity: 55.00% Mismatches: 11
Query Match: 51.27% Indels: 2
DB: Gaps: 1

US-10-010-731-2 (1-45) x AB049718 (1-380)

OY 8 AsPLysTYrRgGLyPRoCYsPhe-----SerGLyCYsAsPThrHiSCysThrThrLys 25
DB 368 AATMAACACTGGGACCATGCATCCAGATGTACTGCACAAACATTGCAGGAACAAC 309
OY 26 GLuAsnaLaValSerGLyARgCYsARgAsPAspPheARgCYsTRPCysThrLysARgCYs 45
DB 308 GAGCACATACAGAGTGGAGGAGGTGCAGGATATTTCCCTGCTGCTGCACCTCGAAGACTGT 249

Search completed: June 21, 2003, 07:19:17
Job time : 1795.65 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 05:36:29 ; Search time 164.647 Seconds
(without alignments)
615.498 Million cell updates/sec

Title: US-10-010-731-2
Perfect score: 275
Sequence: 1 RTCEMLADKYRGPCFSGCDT.....ENAVSGRCRDRCWCTKRC 45

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP=107310010731.ecgn.1.1.338.0runat.17062003.095704.28153 -DSPHLOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	275	100.0	250	19 AAV39187	Alfalfa plant anti
2	275	100.0	490	19 AAV39186	Antifungal polypep
3	275	100.0	507	19 AAV39195	Antifungal polypep
4	241	87.6	327	19 AAV39194	Antifungal polypep
5	231	84.0	200	19 AAV39190	Antifungal polypep
6	214	77.8	468	21 AA249412	Pea Defensin prote
7	206	74.9	494	22 AAD17530	Soybean Gly m2 pro
8	185	67.3	293	19 AAV39191	Antimicrobial Lc-A
9	168	61.1	141	15 AA070126	Antifungal polypep
10	158.5	57.6	138	14 AA038648	Encodes antifungal
11	91	33.1	487	21 AAC34773	Arabidopsis thalia
12	91	33.1	495	21 AAA78455	Plant SDF polynuc
13	91	33.1	552	21 AAA78544	Plant SDF polynuc
14	88	32.0	489	21 AAC44316	Arabidopsis thalia
15	88	32.0	526	21 AAC34077	Arabidopsis thalia
16	87	31.6	510	21 AAC45669	Arabidopsis thalia
17	87	31.6	512	21 AAC32882	Arabidopsis thalia
18	81	29.5	47	19 AAV39197	Antifungal polypep
19	80.5	29.3	823	23 AB116863	Drosophila melanog
20	80.5	29.3	2823	23 AB116862	Drosophila melanog
21	80	29.1	458	24 ABN94581	Gene #1079 used to
22	80	29.1	1546	24 AB054166	Human ovarian anti
23	79.5	28.9	693	15 AA058991	Diospyros texana a
24	78.5	28.5	627	15 AA058992	Diospyros texana a
25	78	28.4	465	21 AAC34026	Arabidopsis thalia
26	78	28.4	520	21 AAC35542	Arabidopsis thalia
27	78	28.4	597	21 AAC40605	Arabidopsis thalia
28	76.5	27.8	363	15 AA070067	Sequence encoding
29	76.5	27.8	492	15 AA070064	Sequence encoding
30	73.5	26.7	499	22 AAAS4398	Plant defensin par
31	73.5	26.7	517	22 AAAS4399	Plant defensin cod
32	72.5	26.4	167	20 AA115805	CDNA encoding the
33	72.5	26.4	236	20 AA115806	CDNA encoding the
34	72.5	26.4	376	23 AB116859	Drosophila melanog
35	72.5	26.4	488	20 AA115804	CDNA encoding dtos
36	72.5	26.4	2376	23 AB116858	Drosophila melanog
37	72	26.2	147	14 AA038649	Encodes antifungal
38	72	26.2	147	15 AA070127	Antimicrobial Ct-A
39	71.5	26.0	219	23 AB116865	Drosophila melanog
40	71.5	26.0	2219	23 AB116864	Drosophila melanog
41	71.5	26.0	2784	23 AB117936	Drosophila melanog
42	71.5	26.0	11043	23 AB128123	Drosophila melanog
43	70.5	25.6	550	21 AA248826	Human deltal codin
44	70.5	25.6	1980	18 AAT59454	H-Delta-1 contig c
45	70.5	25.6	2663	18 AAT70174	Proliferation and

ALIGNMENTS

RESULT 1	AAV39187	standard; DNA; 250 BP.
ID	AAV39187	
XX	AAV39187;	
AC		
XX		
DT	25-SEP-1998 (first entry)	
XX		
DE	Alfalfa plant antifungal polypeptide AlfAlfP1 encoding DNA.	
XX		
KW	Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;	
KW	plant pathogenic fungus; AlfAlfP1; AlfAlfP2; ds.	
XX		
OS	Medicago sativa.	
XX		
FH	key	Location/Qualifiers
FT	CDS	105..242
FT		/*tag= a

FT /product= "mature AlfAFP1"
XX
XX MO9826083-A1.
PN 18-JUN-1998.
XX
PD 11-DEC-1997; 97MO-US22662.
XX
XX 13-DEC-1996; 96US-0766355.
XX
XX (MONS) MONSANTO CO.
PA
XX Hakihi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
PI WPI: 1998-348537/30.
XX P-PSDB; AAW61964.
DR
XX
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
XX
PS Claim 3; Page 78; 97pp; English.
XX
XX This DNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2 are
CC useful to control plant fungi, especially pathogenic fungi, by
CC transforming plant cells with a vector comprising sequences encoding
CC AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
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XX Sequence 250 BP; 73 A; 48 C; 64 G; 65 T; 0 other:
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Alignment Scores:
Pred. No.: 1,78e-25 length: 250
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-10-010-731-2 (1-45) x AAV39186 (1-250)
QY 1 ArgThCysGluAsnLeuAlaAspLysTYrArgGlyProCysPheSerGlyCysAspThr 20
XX
Db 105 AGAACATGTGACAAATTGGCAGATAATATAGGGGACCAATGCTTAGTGGTTGTGACACT 164
XX
QY 21 HisCysThrThyGluAsnAlaValSerGlyArgCysArgAspPheArgCysTrp 40
XX
Db 165 CACTGCACAACCAAAAGACGACGTAGTGAAGGTGTAGGAGCAGACTCCCTCTGTG 224
XX
QY 41 CysThrLysArgCys 45
XX
Db 225 TGTACTAAAGATGT 239
XX
RESULT 2
AAV39186 standard; DNA: 490 BP.
ID
XX
AC AAV39186;

XX
XX 01-OCT-1998 (first entry)
DT
XX Antifungal polypeptide AlfAFP1 encoding cDNA.
XX
DE Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance:
XX plant pathogenic fungus; AlfAFP1; AlfAFP2; ss.
KW
XX Medicago sativa.
OS
FH Key Location/Qualifiers
FT CDS 75..293
FT /*tag= a
FT /transl_except= (pos:129..131, aa:Glu)
FT /product= "AlfAFP1 polypeptide"
FT sig_peptide 75..155
FT /*tag= b
FT mat_peptide 156..290
FT /*tag= c
XX
XX
XX MO9826083-A1.
XX
XX 18-JUN-1998.
PD
XX
XX 11-DEC-1997; 97MO-US22662.
XX
XX 13-DEC-1996; 96US-0766355.
XX
XX (MONS) MONSANTO CO.
PA
XX Hakihi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
PI WPI: 1998-348537/30.
XX P-PSDB; AAW61967.
DR
XX
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
XX
PS Claim 5; Fig 1; 97pp; English.
XX
XX This cDNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2 are
CC useful to control plant fungi, especially pathogenic fungi, by
CC transforming plant cells with a vector comprising sequences encoding
CC AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
XX Sequence 490 BP; 182 A; 85 C; 85 G; 136 T; 2 other:
SQ
Alignment Scores:
Pred. No.: 4.07e-25 length: 490
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-10-010-731-2 (1-45) x AAV39186 (1-490)

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QY      1 ArgThrcysgluasnleualaspIysTyArgGlyProCysPheSerGlyCysAspThr 20
Db      156 AGAACATGTGAGATTGGCAGATTAATATAGGGGACCACTGTTAGTGGTTGGACACT 215
QY      21 HisCysThrThrluysgluasnAlaIaValSerGlyArGcysArGspAspPheArGcysTyr 40
Db      216 CACTGCACACCAACCAAGAGACGAGTTAGTGAAGGTGTAGGACGACACTCCGCTGCTGG 275
QY      41 CysThrLysArGcys 45
Db      276 TGTACTAAAGATGT 290

RESULT 3
AAV39195
ID      AAV39195 standard; DNA: 507 BP.
AC      AAV39195;
DE      25-SEP-1998 (first entry)
XX      Antifungal polypeptide AlfAP1 mature sequence encoding DNA.
XX      Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance:
XX      plant pathogenic fungus; AlfAP1; AlfAFP2; ds.
XX      Medicago sativa.
XX      Key      Location/Qualifiers
XX      CDS      173..310
XX      FT      /*tag= a
XX      FT      /product= "mature AlfAP1"
XX      PN      WO9826083-A1.
XX      PD      18-JUN-1998.
XX      PF      11-DEC-1997; 97WO-US22662.
XX      PR      13-DEC-1996; 96US-0766355.
XX      PA      (MONS ) MONSANTO CO.
XX      PI      Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX      DR      WPI: 1998-348537/30.
XX      DR      P-PSDB; AAW61964.
XX      PT      Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
XX      PT      - used to control plant pathogenic fungi and to produce transformed
XX      PT      plants with increased fungal resistance
XX      PS      Claim 5; Page 77; 97pp; English.
XX      CC      This DNA encodes an antifungal polypeptide, AlfAP1 isolated from
XX      CC      alfalfa plants (Medicago). The polypeptides AlfAP1 and AlfAFP2 are
XX      CC      useful to control plant fungi, especially pathogenic fungi, by
XX      CC      transforming plant cells with a vector comprising sequences encoding
XX      CC      AlfAP1 or AlfAP2 to allow expression of antifungally effective amounts
XX      CC      of the polypeptide. Such transformed plants may be e.g. apple, wheat,
XX      CC      cotton and especially potato. Micro-organisms may also be transformed
XX      CC      to produce the polypeptides, and applied to plants to control plant
XX      CC      fungi. The polypeptides can also be included with a suitable solvent in
XX      CC      antifungal compositions and these can be administered to plants to
XX      CC      control plant fungi. Such compositions and genetically engineered plants
XX      CC      may also contain additional molecules e.g. the compositions can contain
XX      CC      other antifungal agents or the plants contain DNA encoding insecticidal
XX      CC      (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
XX      CC      to prepare antibodies useful to detect polypeptides or isolate other
XX      CC      alfalfa plant antifungal protein antigens. The nucleic acids are useful
XX      CC      to produce polypeptides and transgenic plants and as probes or primers in
XX      CC      nucleic acid hybridisation e.g. to detect complementary sequences in
XX      CC      samples, and to prepare mutants or isolate similar sequences from related
```

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CC      species.
XX      SQ      Sequence 507 BP: 181 A; 85 C; 102 G; 136 T; 3 other;
XX      Alignment Scores:
XX      Pred. No.:      4.25e-25
XX      Score:      275.00
XX      Percent Similarity: 100.00%
XX      Best local Similarity: 100.00%
XX      Query Match:      100.00%
XX      DB:      19
XX      Gaps:      0
XX      US-10-010-731-2 (1-45) x AAV39195 (1-507)
QY      1 ArgThrcysgluasnleualaspIysTyArgGlyProCysPheSerGlyCysAspThr 20
Db      173 AGAACATGTGAGATTGGCAGATTAATATAGGGGACCACTGTTAGTGGTTGGACACT 232
QY      21 HisCysThrThrluysgluasnAlaIaValSerGlyArGcysArGspAspPheArGcysTyr 40
Db      233 CACTGCACACCAACCAAGAGACGAGTTAGTGAAGGTGTAGGACGACACTCCGCTGCTGG 292
QY      41 CysThrLysArGcys 45
Db      293 TGTACTAAAGATGT 307

RESULT 4
AAV39194
ID      AAV39194 standard; DNA: 327 BP.
AC      AAV39194;
DE      25-SEP-1998 (first entry)
XX      Antifungal polypeptide AlfAFP2 3' region.
XX      Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance:
XX      plant pathogenic fungus; AlfAP1; AlfAFP2; ds.
XX      Medicago sativa.
XX      PN      WO9826083-A1.
XX      PD      18-JUN-1998.
XX      PF      11-DEC-1997; 97WO-US22662.
XX      PR      13-DEC-1996; 96US-0766355.
XX      PA      (MONS ) MONSANTO CO.
XX      PI      Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX      DR      WPI: 1998-348537/30.
XX      PT      Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
XX      PT      - used to control plant pathogenic fungi and to produce transformed
XX      PT      plants with increased fungal resistance
XX      PS      Claim 18; Page 77; 97pp; English.
XX      CC      This sequence represents the 3' region of the DNA encoding an antifungal
XX      CC      polypeptide, AlfAP2 isolated from alfalfa plants (Medicago). The
XX      CC      polypeptides AlfAP1 and AlfAFP2 are useful to control plant fungi,
XX      CC      especially pathogenic fungi, by transforming plant cells with a vector
XX      CC      comprising sequences encoding AlfAP1 or AlfAFP2 to allow expression of
XX      CC      antifungally effective amounts of the polypeptide. Such transformed
XX      CC      plants may be e.g. apple, wheat, cotton and especially potato.
XX      CC      Micro-organisms may also be transformed to produce the polypeptides, and
XX      CC      applied to plants to control plant fungi. The polypeptides can also be
XX      CC      included with a suitable solvent in antifungal compositions and these can
XX      CC      be administered to plants to control plant fungi. Such compositions and
XX      CC      genetically engineered plants may also contain additional molecules e.g.
```

CC the compositions can contain other antifungal agents or the plants
 CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)
 CC proteins. The polypeptides are also useful to prepare antibodies useful
 CC to detect polypeptides or isolate other alfalfa plant antifungal protein
 CC antigens. The nucleic acids are useful to produce polypeptides and
 CC transgenic plants and as probes or primers in nucleic acid hybridisation
 CC e.g. to detect complementary sequences in samples, and to prepare mutants
 CC or isolate similar sequences from related species.

XX
 SQ Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	4.02e-21	327	241.00	41		
Percent Similarity:	97.62%		0			
Best Local Similarity:	97.62%		1			
Query Match:	87.64%		0			
DB:	19					

US-10-010-731-2 (1-45) x AAV39194 (1-327)

OY 4 GluasnleuAlaaspLysTyrArgGlyProCysPheSerGlyCysAspThrHisCysThr 23

DB 1 GAGATTGGCGGATAGTAATAGGGGACCAATGCTTTAGTGTGTGACACTCAGTGCACA 60

OY 24 ThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTyrCysThrLys 43

DB 61 ACCAAGAGAGAACGAGTGTAGTGAAGGTGTAGGATGACTTTCCTTTAGTGTACTTAA 120

OY 44 ArgCys 45

DB 121 AGATGT 126

RESULT 5

AAV39190

AAV39190;

25-SEP-1998 (first entry)

XX Antifungal polypeptide AlfaFP2 5' region.

XX Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;

XX plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.

XX Medicago sativa.

XX WO9826083-A1.

XX 18-JUN-1998.

XX 11-DEC-1997; 97WO-US22662.

XX 13-DEC-1996; 96US-0766355.

XX (MONS) MONSANTO CO.

XX Hekiml S, Liang J, Rosenberger CA, Shah DM, Wu YS;

XX WPI; 1998-348537/30.

XX Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)

XX - used to control plant pathogenic fungi and to produce transformed

XX plants with increased fungal resistance

XX Claim 18; Page 75; 97pp; English.

XX This sequence represents the 5' region of the DNA encoding an antifungal

XX polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The

XX polypeptides AlfaFP1 and AlfaFP2 are useful to control plant fungi,

XX especially pathogenic fungi, by transforming plant cells with a vector

CC antifungally effective amounts of the polypeptide. Such transformed

CC plants may be e.g. apple, wheat, cotton and especially potato.

CC Micro-organisms may also be transformed to produce the polypeptides, and

CC applied to plants to control plant fungi. The polypeptides can also be

CC included with a suitable solvent in antifungal compositions and these can

CC be administered to plants to control plant fungi. Such compositions and

CC genetically engineered plants may also contain additional molecules e.g.

CC the compositions can contain other antifungal agents or the plants

CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)

CC proteins. The polypeptides are also useful to prepare antibodies useful

CC to detect polypeptides or isolate other alfalfa plant antifungal protein

CC antigens. The nucleic acids are useful to produce polypeptides and

CC transgenic plants and as probes or primers in nucleic acid hybridisation

CC e.g. to detect complementary sequences in samples, and to prepare mutants

CC or isolate similar sequences from related species.

XX
 SQ Sequence 200 BP; 48 A; 36 C; 65 G; 50 T; 1 other:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	3.79e-20	200	231.00	39		
Percent Similarity:	100.00%		0			
Best Local Similarity:	100.00%		0			
Query Match:	84.00%		0			
DB:	19					

US-10-010-731-2 (1-45) x AAV39190 (1-200)

OY 1 ArgThrCysGluAsnLeuAlaaspLysTyrArgGlyProCysPheSerGlyCysAspThr 20

DB 80 AGAACATGTGAGATTTGGCAGATTAATATAGGGGACCAATGCTTTAGTGTGTGACACT 139

OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39

DB 140 CACTGCACACCAACAGACGAGTGTAGTGAAGGTGTAGGGGACCACTTCCCTGC 196

RESULT 6

AAZ49412

AAZ49412 standard; cDNA; 468 BP.

XX AAZ49412;

XX 04-APR-2000 (first entry)

XX Pea Defensin protein Drr230, encoding cDNA.

XX Transgenic plant; disease resistance; DRR206; defensin; Drr230; PR10.1;

XX chitinase; recombinant expression system; Pea; Canola; Blackleg fungus;

XX CanV 35S inducible promoter; T-DNA; bacterial/fungal pathogen;

XX Leptosphaeria maculans; Rhizoctonia solani; Sclerotinia sclerotiorum; ds.

XX Pisum sativum.

XX Key

XX CDS

XX WO200001824-A2.

Location/Qualifiers

/*tag= a

/product= "Pea Defensin protein, Drr230"

/note= "Confers resistance against fungal and bacterial

pathogens"

XX 02-JUL-1999; 99WO-CA00608.

XX 03-JUL-1998; 98CA-2242116.

XX 06-JUL-1998; 98US-0091751.

XX (UYMA-) UNIV MANITOBA.

XX Frlstensky B, Wang Y;

XX

OS Medicago sativa.
XX
PN MO9826083-AL.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97MO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
DR WPI; 1998-348537/30.
XX
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
XX plants with increased fungal resistance
XX
PS Claim 18; Page 75; 97pp; English.

CC This represents a coding sequence of an antifungal polypeptide, AlfAP2
CC isolated from alfalfa plants (Medicago). The polypeptides AlfAP1 and
CC AlfAP2 are useful to control plant fungi, especially pathogenic fungi,
CC by transforming plant cells with a vector comprising sequences encoding
CC AlfAP1 or AlfAP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 293 BP; 82 A; 60 C; 72 G; 77 T; 2 other;

Alignment Scores:

Pred. No.:	3,01e-14	Length:	293
Score:	185.00	Matches:	30
Percent Similarity:	86.84%	Conservative:	3
Best Local Similarity:	78.95%	Mismatches:	5
Query Match:	67.27%	Indels:	0
DB:	19	Gaps:	0

US-10-010-731-2 (1-45) x AAV39191 (1-293)

QY 2 ThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThrHis 21
Db 176 ACTTGAGCAATTTGGCTACATACAGGACCATGCTTCGGTGTGACTTCAC 235
QY 22 CysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39
Db 236 TGC AAAACCAAGACACTTACTTACGCGNAGGTGACGAGCAGCTTCGCTGC 289

RESULT 9

AAO70126
ID AAO70126 standard; cDNA; 141 BP.
XX
AC AAO70126;
XX
DT 14-FEB-1995 (first entry)
XX
DE Antimicrobial LC-AFP.
XX

KM Antimicrobial; LC-AFP; symbiosis; disease-resistance;
KM fungus-resistance; Clavibacter xyl subsp. cynodontis; Cxc;
KM crop improvement; endophyte; ss.

OS Lathyrus cicerca.
XX
PN MO9416076-A.
XX
PD 21-JUL-1994.
XX

PF 05-JAN-1994; 94MO-GB00012.
XX
PR 08-JAN-1993; 93GB-0000281.
XX
PA (ZENE) ZENECA LTD.
XX

PI Dubock AC, Powell KA, Rees SB;
XX
DR WPI; 1994-249223/30.
XX
DR P-PSDB; AAR57322.
XX

PT Antimicrobial protein producing endo-symbiotic microorganisms -
PT is produced by combining nucleic acids encoding the protein with
PT an endophyte, useful for protecting plant hosts from esp. fungal
XX disease
XX
PS Disclosure; Page 30; 39pp; English.

CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyl subsp. cynodontis (Cxc). Plants or seeds treated
CC with recombinant Cxc are protected against fungal disease. A
CC suitable antimicrobial protein is LC-AFP from L. cicerca. A
CC possible predicted sequence for the LC-AFP gene is given in AAO70126.
XX

SQ Sequence 141 BP; 43 A; 30 C; 32 G; 33 T; 3 other;

Alignment Scores:

Pred. No.:	1.56e-12	Length:	141
Score:	168.00	Matches:	25
Percent Similarity:	70.21%	Conservative:	8
Best Local Similarity:	53.19%	Mismatches:	12
Query Match:	61.09%	Indels:	2
DB:	15	Gaps:	1

US-10-010-731-2 (1-45) x AAO70126 (1-141)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18
Db 1 AAGACTTGGGAGAACCTTCTGCACTTCACAGGACCATGCTTCAGATGCAAACTGC 60
QY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
Db 61 AACACACATTGGCAAGAACACAGCAGCATCTTCTTCTGGAAGATGACAGATGATTTCCNN 120

QY 39 CysTrpCysThrLysArgCys 45

Db 121 TCGTGGTGCACCTAGAAACTGC 141

RESULT 10

AAO38648
ID AAO38648 standard; DNA; 138 BP.
XX
AC AAO38648;
XX

DT 07-JUL-1993 (first entry)

DE Encodes antifungal protein LC-AFP1.

XX
KM Raphanus sativus; Brassica; Arabidopsis; Citrus; Lathyrus; Cilloria;
KM fungicide; bacteriocide; antibiotic; antifungal; gram positive;
KM plant disease resistance; low toxicity.
XX
OS Lathyrus cicerca.


```
XX Key Location/Qualifiers
FH CDS 1..138
FT /*tag= a
XX
XX W09305153-A.
XX
XX 18-MAR-1993.
XX
XX 27-AUG-1992; 92WO-GB01570.
XX
XX 29-AUG-1991; 91GB-0018523.
XX
XX 13-FEB-1992; 92GB-0003038.
XX
XX 25-JUN-1992; 92GB-0013526.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
XX Vanderleyden J;
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica
XX or dahlia, useful for increasing plants' resistance to fungal and
XX bacterial diseases
XX
XX PS Disclosure; Fig 31A; 110pp; English.
XX
XX CC This sequence appears to encode antifungal protein Lc-Appl from
XX Lathyrus ciceria - see AAR33760. The exact source and isolation of the
XX sequence is unclear from the specification.
XX
XX SQ Sequence 138 BP; 43 A; 30 C; 32 G; 33 T; 0 other;

Alignment Scores:
Pred. NO: 2.28e-11 Length: 138
Score: 158.50 Matches: 25
Percent Similarity: 70.21% Conservative: 8
Best Local Similarity: 53.19% Mismatches: 11
Query Match: 57.64% Indels: 3
DB: 14 Gaps: 2

US-10-010-731-2 (1-45) x AAC38648 (1-138)

OY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgLysProCysPhe-----SerGlyCys 18
   ::::::::::::::::::::::::::::
DB 1 AAGCACTGCGAGAACCTTTCTGGAACCTTCAAGGACCATCCATCCAGATGAAACTGC 60
   ::::::::::::::::::::::::::::::

OY 19 AspPThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspPheArg 38
   ::::::::::::::::::::::::::::
DB 61 AACAAAGCATTCGACAGAACACAGACAGCATCTCTTCTGCAAGATGACAGATGATTC--- 117
   ::::::::::::::::::::::::::::

OY 39 CysTrpCysThrLysArgCys 45
   ::::::::::::::::::::::::::::
DB 118 TGCTGCTGCACACTAGAAACTGC 138
   ::::::::::::::::::::::::::::

RESULT 11
AAC34773
ID AAC34773 standard; DNA; 487 BP.
XX
XX AAC34773:
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 7837.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX
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XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX
XX 05-MAR-1999; 99US-0121180.
XX
XX 09-MAR-1999; 99US-0123548.
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XX 23-MAR-1999; 99US-0125788.
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XX 25-MAR-1999; 99US-0126264.
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XX 29-MAR-1999; 99US-0126785.
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XX 06-APR-1999; 99US-0128234.
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XX 08-APR-1999; 99US-0128714.
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XX 16-APR-1999; 99US-0129845.
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XX 24-JUN-1999; 99US-0140695.
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XX 28-JUN-1999; 99US-0140823.
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XX 29-JUN-1999; 99US-0140991.
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XX 30-JUN-1999; 99US-0141287.
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XX 01-JUL-1999; 99US-0141842.
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XX 01-JUL-1999; 99US-0142154.
XX
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	PR	12-JUL-1999;	99US-0142977.
	PR	13-JUL-1999;	99US-0143542.
	PR	14-JUL-1999;	99US-0143624.
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	PR	19-JUL-1999;	99US-0144325.
	PR	19-JUL-1999;	99US-0144331.
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	PR	28-JUL-1999;	99US-0145951.
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	PR	02-AUG-1999;	99US-0146388.
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	PR	03-AUG-1999;	99US-0147038.
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	PR	05-AUG-1999;	99US-0147302.
	PR	05-AUG-1999;	99US-0147192.
	PR	06-AUG-1999;	99US-0147260.
	PR	06-AUG-1999;	99US-0147303.
	PR	06-AUG-1999;	99US-0147416.
	PR	09-AUG-1999;	99US-0147493.
	PR	09-AUG-1999;	99US-0147935.
	PR	10-AUG-1999;	99US-0148171.
	PR	11-AUG-1999;	99US-0148319.
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	PR	20-AUG-1999;	99US-0149929.
	PR	23-AUG-1999;	99US-0149902.
	PR	23-AUG-1999;	99US-0149930.
	PR	25-AUG-1999;	99US-0150566.
	PR	26-AUG-1999;	99US-0150884.
	PR	27-AUG-1999;	99US-0151065.
	PR	27-AUG-1999;	99US-0151066.
	PR	27-AUG-1999;	99US-0151080.
	PR	30-AUG-1999;	99US-0151303.
	PR	31-AUG-1999;	99US-0151438.
	PR	01-SEP-1999;	99US-0151930.
	PR	07-SEP-1999;	99US-0152363.
	PR	10-SEP-1999;	99US-0153070.
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	PR	04-OCT-1999;	99US-0157171.
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	PR	06-OCT-1999;	99US-0157865.
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	PR	13-OCT-1999;	99US-0159294.
	PR	13-OCT-1999;	99US-0159295.
	PR	14-OCT-1999;	99US-0159329.
	PR	14-OCT-1999;	99US-0159330.
	PR	14-OCT-1999;	99US-0159331.
	PR	14-OCT-1999;	99US-0159637.
	PR	14-OCT-1999;	99US-0159638.
	PR	18-OCT-19	

XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 42412.
DE
XX Hybridisation assay: genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS
XX EPI033405-A2.
PN
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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PR 18-JUN-1999; 99US-0139457.
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PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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Best Local Similarity: 38.30%
Conservative: 9
Mismatch: 16
Query Match: 32.00%
Indels: 4
DB: 21
Gaps: 3

US-10-010-731-2 (1-45) x AAC34077 (1-526)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 06:15:24 ; Search time 35.4706 Seconds
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389.068 Million cell updates/sec

Title: US-10-010-731-2

Perfect score: 275

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Fgapop 10.0, Fgapext 0.5
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	275	100.0	250	4	US-09-003-198A-13
3	275	100.0	250	4	US-09-428-805-13
4	275	100.0	480	4	US-09-003-198A-19
5	275	100.0	507	3	US-08-766-355-10
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20	168	61.1	141	4	US-08-971-982-35	Sequence 35, Appli
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26	76.5	27.8	492	1	US-08-543-238-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-08-766-355-13
Sequence 13, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Heterewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-766-355-13

Alignment Scores:
Pred. No.: 2,76e-27 length: 250
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Caps: 0

US-10-010-731-2 (1-45) x US-08-766-355-13 (1-250)

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RESULT 2

US-09-003-198A-13
Sequence 13, Application US/09003198A
Patent No. 6316407

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-09-003-198A-13

Alignment Scores:

Pred. No.: 2,76e-27 length: 250
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 3

US-09-428-805-13
Sequence 13, Application US/09428805
Patent No. 6329504

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
TELEFAX: (512) 418-3000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-09-428-805-13

Alignment Scores:

Pred. No.: 2,76e-27 length: 250
Score: 275.00 Matches: 45

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-428-805-13 (1-250)

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225 TGTACTAAAGATGT 239

RESULT 4.

US-09-003-198A-19

Sequence 19, Application US/09003198A

Patent No. 6316407

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip Maganlal

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Hakim, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,198A

FILING DATE: 07-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 490 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-09-003-198A-19

Alignment Scores:

Pred. No.: 6,41e-27

Score: 275.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 4

US-10-010-731-2 (1-45) x US-09-003-198A-19 (1-490)

QY 1 ArgThrCysGluAsnLeuAlaAspIlySTyArgGlyProCysPheSerGlyCysAspThr 20
156 AGACATGTGAGATTTGGCAGATAATATAGGGGACCATGCTTAGTGTGTGACACT 215

QY 21 HisCysThrThrllysGluAsnAlaValSerGlyArgCysArgAspSphearGcystp 40
216 CACTGCACAACCAAGAACAGCAGTTAGTGAAGGTGTAGGACGACTTCGCTGCG 275

DB 41 CysThrIysArgCys 45
276 TGTACTAAAGATGT 290

RESULT 5

US-08-766-355-10

Sequence 10, Application US/08766355

Patent No. 6121436

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip Maganlal

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Hakim, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 77210

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/766,355

FILING DATE: Concurrently Herewith

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: MOBT:063

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: modified_base

LOCATION: one-of(17, 424, 485)

OTHER INFORMATION: /mod_base= OTHER

OTHER INFORMATION: /note= "N = A or C or G or T"

US-08-766-355-10

Alignment Scores:

Pred. No.: 6,69e-27

Score: 275.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 3

US-10-010-731-2 (1-45) x US-08-766-355-10 (1-507)

QY 1 ArgThrCysGluAsnLeuAlaAspIlySTyArgGlyProCysPheSerGlyCysAspThr 20

Db 173 AGAACATGTCAGAAATTTGGCAGATTAATATATAGGGGACCACATGCTTAACTGCTTGACACT 232
QY 21 HiscysThrThrylsgluAsnAlaValserGlyArgCysArgAspAspPheArgCysTrp 40
|||||
Db 233 CACTGCACAACCAAGAGAACGACGTTAGTGAAGGTGTAGGACACGACTTCCGCTGCTGG 292
QY 41 CysThrllysArgCys 45
|||||
Db 293 TGTACTATAAAGATGT 307

RESULT 6

US-09-003-198A-10
; Sequence 10, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-Jan-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: one-of(17, 424, 485)
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-003-198A-10

US-09-003-198A-10

Alignment Scores:
Pred. No.: 6,69e-27 Length: 507
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-003-198A-10 (1-507)

QY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
|||||
Db 173 AGAACATGTCAGAAATTTGGCAGATTAATATATAGGGGACCACATGCTTAACTGCTTGACACT 232

QY 21 HiscysThrThrylsgluAsnAlaValserGlyArgCysArgAspAspPheArgCysTrp 40
|||||
Db 233 CACTGCACAACCAAGAGAACGACGTTAGTGAAGGTGTAGGACACGACTTCCGCTGCTGG 292
QY 41 CysThrllysArgCys 45
|||||
Db 293 TGTACTATAAAGATGT 307

RESULT 7

US-09-428-805-10
; Sequence 10, Application US/09428805
; Patent No. 6329504
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/428,805
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,355
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: one-of(17, 424, 485)
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-428-805-10

US-09-428-805-10

Alignment Scores:
Pred. No.: 6,69e-27 Length: 507
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-428-805-10 (1-507)

QY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
|||||
Db 173 AGAACATGTCAGAAATTTGGCAGATTAATATATAGGGGACCACATGCTTAACTGCTTGACACT 232

OY 21 HsCysThrThLySGluAsnAlaValSerGlyArgCysArGAspPheArgCysTrp 40
|||||
Db 233 CACTGCACAACCAAGAGACGACGATTAGTGAAGGTGTAGGACACGACTTCGCTGCTG 292

OY 41 CysThrLyArgCys 45
|||||
Db 293 TGTACTMAAAGATGT 307

RESULT 8

US-08-766-355-9
; Sequence 9, Application US/08766355
; Patent No. 6121436
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,355
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ. ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: one-of(244, 305)
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-08-766-355-9

Alignment Scores:
Pred. No.: 8, 87e-23 Length: 327
Score: 241.00 Matches: 41
Percent Similarity: 97.62% Conservative: 0
Best Local Similarity: 97.62% Mismatches: 1
Query Match: 87.64% Indels: 0
DB: 3 Gaps: 0

US-10-010-731-2 (1-45) x US-08-766-355-9 (1-327)

OY 4 GluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThrHisCysThr 23
|||||
Db 1 GAGAAATTTGGCGGATAGTATAGGAGACCATGCTTTAGTGTGTGACACTGCTGACACA 60
OY 24 ThrLySGluAsnAlaValSerGlyArgCysArGAspPheArgCysTrpCysThrLyS 43

Db 61 ACCAAGAGAACCCAGTACTAGTGAAGGTGTAGGAGATGACTTGTGTTAGTACTAA 120
|||||

OY 44 ArgCys 45
|||||
Db 121 AGATGT 126

RESULT 9

US-09-003-198A-9
; Sequence 9, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ. ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: one-of(244, 305)
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-003-198A-9

Alignment Scores:
Pred. No.: 8, 87e-23 Length: 327
Score: 241.00 Matches: 41
Percent Similarity: 97.62% Conservative: 0
Best Local Similarity: 97.62% Mismatches: 1
Query Match: 87.64% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-003-198A-9 (1-327)

OY 4 GluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThrHisCysThr 23
|||||
Db 1 GAGAAATTTGGCGGATAGTATAGGAGACCATGCTTTAGTGTGTGACACTGCTGACACA 60
OY 24 ThrLySGluAsnAlaValSerGlyArgCysArGAspPheArgCysTrpCysThrLyS 43
|||||
Db 61 ACCAAGAGAACCCAGTACTAGTGAAGGTGTAGGAGATGACTTGTGTTAGTACTAA 120
|||||

OY 44 ArgCys 45
|||||
Db 121 AGATGT 126

RESULT 10

US-09-428-805-9
; Sequence 9, Application US/09428805
; Patent No. 6329504
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/428,805
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,355
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-5000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: one-of(244, 305)
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N - A or C or G or T"
US-09-428-805-9

Alignment Scores:

Pred. No.:	8.87e-23	Length:	327
Score:	241.00	Matches:	41
Percent Similarity:	97.62%	Conservative:	0
Best Local Similarity:	97.62%	Mismatches:	1
Query Match:	87.64%	Indels:	0
DB:	4	Gaps:	0

US-10-010-731-2 (1-45) x US-09-428-805-9 (1-327)

OY 4 GluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThrHisCysThr 23
|||||
Db 1 GAGAAATTGGCGGATAGATAGGACCATGCTTAGTGCTGACACTCAGTCACACA 60
OY 24 ThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysThrLys 43
|||||

Db 61 ACCAAGAGAACGCGACTAGTAGAGGTGTAGGATGACTTTGTTAGTGTACTAAA 120
OY 44 ArgCys 45
|||||
Db 121 AGATGT 126

RESULT 11

US-09-003-198A-18
; Sequence 18, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-003-198A-18

Alignment Scores:

Pred. No.:	7.38e-22	Length:	189
Score:	231.50	Matches:	40
Percent Similarity:	97.56%	Conservative:	0
Best Local Similarity:	97.56%	Mismatches:	0
Query Match:	84.18%	Indels:	1
DB:	4	Gaps:	1

US-10-010-731-2 (1-45) x US-09-003-198A-18 (1-189)

OY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
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Db 63 AGAACATGTGAGAAATTGGGAGATTAATATAGGCGACCATGCTTAGTGCTGTGACACT 122
OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg---Cys 39
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Db 123 CACTGCACAACCAAGAGAACGCGAGTTAGTGAAGGTGTAGGAGCAGACTTCGCTGCTGC 182
OY 40 Trp 40
|||
Db 183 TGG 185
RESULT 12

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US-08-766-355-5
: Sequence 5, Application US/08766355
: Patent No. 6121436
: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Meganalal
: APPLICANT: Wu, Yonie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakim, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 77210
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/766,355
: FILING DATE: Concurrently Herewith
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Mitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: MOBT:063
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 200 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: 17
: OTHER INFORMATION: /mod_base= OTHER
: OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-5

Alignment Scores:
Pred. No.: 9,19e-22 Length: 200
Score: 231.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 3 Gaps: 0

US-10-010-731-2 (1-45) x US-08-766-355-5 (1-200)
OY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
Db 80 AGACATGTCAGATTTGGCAGATAAATATAGGGGACCATCTTAGTGTTGACACT 139
OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39
Db 140 CACTGCACACCAAGAGAACGCGAGTAGTGGAAGGTGTAGGAGCGACTTCCGCTGC 196

RESULT 13
: Sequence 5, Application US/09003198A
: Patent No. 6316407
: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Meganalal

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: APPLICANT: Wu, Yonie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakim, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/003,198A
: FILING DATE: 07-JAN-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Paterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT:193
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713) 787-1400
: TELEFAX: (713) 787-1440
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 200 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: 17
: OTHER INFORMATION: /mod_base= OTHER
: OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-003-198A-5

Alignment Scores:
Pred. No.: 9,19e-22 Length: 200
Score: 231.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-003-198A-5 (1-200)
OY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
Db 80 AGACATGTCAGATTTGGCAGATAAATATAGGGGACCATCTTAGTGTTGACACT 139
OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39
Db 140 CACTGCACACCAAGAGAACGCGAGTAGTGGAAGGTGTAGGAGCGACTTCCGCTGC 196

RESULT 14
: Sequence 5, Application US/09428805
: Patent No. 6329504
: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Meganalal
: APPLICANT: Wu, Yonie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakim, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: NUMBER OF SEQUENCES: 14

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 17
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-428-805-5

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 4 Gaps: 0

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QY 21 HisGysThrThrlysgluasnAlaValSerGlyArgGlyCysArgAspPheArgCys 39
Db 140 CACTGCACACCAAGACGAGTGTAGGAGGTGTAGGAGCAGACTTCGCTGC 196

RESULT 15
US-08-766-355-6
Sequence 6, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
```

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CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
TELEFAX: (512) 418-3000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-6

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Query Match: 67.27% Indels: 0
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QY 22 CysThrThrlysgluasnAlaValSerGlyArgGlyCysArgAspPheArgCys 39
Db 236 TGCAAAACCAAGACACTTACTTAGCGNAGGTGACGAGCAGCACTCCCTGC 289

Search completed: June 21, 2003, 07:53:49
Job time : 40.4706 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 07:19:24 ; Search time 110.118 Seconds
(without alignments)
599.670 Million cell updates/sec

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Perfect score: 275
Sequence: 1 RTCEMLADYRGPCFSGCDF.....ENAVSGRCDPFCMCKTKRC 45

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Searched: 1042519 segs, 733713590 residues
Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

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3	275	100.0	507	9	US-10-010-731-10
4	241	87.6	327	9	US-10-010-731-9

5	231.5	84.2	189	9	US-10-010-731-18	Sequence 18, App1
6	231	84.0	200	9	US-10-010-731-5	Sequence 5, App1
7	206	74.9	461	9	US-10-178-213-451	Sequence 451, App1
8	206	74.9	494	9	US-09-805-694B-5	Sequence 5, App1
9	205.5	74.7	420	9	US-10-178-213-436	Sequence 436, App1
10	203	73.8	563	9	US-10-178-213-439	Sequence 439, App1
11	185	67.3	293	9	US-10-010-731-6	Sequence 6, App1
12	168	61.1	141	10	US-09-759-584-35	Sequence 35, App1
13	157.5	57.3	464	9	US-10-178-213-379	Sequence 379, App1
14	104	37.8	635	9	US-10-178-213-37	Sequence 37, App1
15	103	37.5	222	10	US-09-878-574-10791	Sequence 10791, A
16	103	37.5	277	10	US-09-878-574-11794	Sequence 11794, A
17	103	37.5	361	10	US-09-878-574-1139	Sequence 1139, A
18	103	37.5	466	9	US-10-178-213-385	Sequence 385, App
19	102	37.1	504	9	US-10-178-213-409	Sequence 409, App
20	100.5	36.5	573	9	US-10-178-213-403	Sequence 403, App
21	100	36.4	275	10	US-09-878-574-14296	Sequence 14296, A
22	98	35.6	425	9	US-10-178-213-325	Sequence 325, App
23	98	35.6	587	9	US-10-178-213-331	Sequence 331, App
24	97	35.3	469	9	US-10-178-213-433	Sequence 433, App
25	97	35.3	523	9	US-10-178-213-412	Sequence 412, App
26	97	35.3	553	9	US-10-178-213-340	Sequence 340, App
27	96	34.9	445	9	US-10-178-213-343	Sequence 343, App
28	96	34.9	459	9	US-10-178-213-334	Sequence 334, App
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31	91	33.1	448	9	US-10-178-213-337	Sequence 337, App
32	91	33.1	478	9	US-10-178-213-307	Sequence 307, App
33	90	32.7	557	9	US-10-178-213-28	Sequence 28, App1
34	89.5	32.5	264	10	US-09-878-574-13620	Sequence 13620, A
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37	88	32.0	465	9	US-10-178-213-34	Sequence 34, App1
38	88	32.0	507	9	US-10-178-213-70	Sequence 70, App1
39	88	32.0	534	9	US-10-178-213-103	Sequence 103, App
40	87.5	31.8	441	9	US-10-178-213-106	Sequence 106, App
41	87	31.6	234	9	US-09-938-842A-617	Sequence 617, App
42	87	31.6	468	9	US-10-178-213-97	Sequence 97, App
43	87	31.6	524	9	US-10-178-213-442	Sequence 442, App
44	86	31.3	363	9	US-10-178-213-124	Sequence 124, App
45	86	31.3	367	9	US-10-178-213-121	Sequence 121, App

ALIGNMENTS

RESULT 1
US-10-010-731-13
; Sequence 13, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonle S.
Rosenberger, Cindy A.
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010.731

FILING DATE: 13-NO. US20030041347A1-2001

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
REGISTRATION NUMBER: 33,062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-010-731-13

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Pred. No.: 6,25e-30 Length: 250
Score: 275.00 Matches: 45
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 41 CysThrLysArgCys 45
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RESULT 2
US-10-010-731-19
Sequence 19, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Meganalal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
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FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
REGISTRATION NUMBER: 33,062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-010-731-19

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Pred. No.: 1,46e-29 Length: 490
Score: 275.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 21 HisCysThrHrlyrYsgLuAsnAlaValSerGlyArgCysArgAspPheArgCysTrp 40
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QY 41 CysThrLysArgCys 45
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DB 276 TGTACTTAAAGATGT 290

RESULT 3
US-10-010-731-10
Sequence 10, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Meganalal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
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APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-010-731-18

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Pred. No.: 5.27e-24 Length: 189
Score: 231.50 Matches: 40
Percent Similarity: 97.56% Conservative: 0
Best Local Similarity: 97.56% Mismatches: 0
Query Match: 84.18% Indels: 1
DB: 9 Gaps: 1

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QY 40 Trp 40
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DB 183 TGG 185

RESULT 6
US-10-010-731-5
Sequence 5, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-No. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 17
OTHER INFORMATION: /mod_base= OTHER
/note= "N" = A or C or G or T"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-731-5

Alignment Scores:
Pred. No.: 6.65e-24 Length: 200
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 9 Gaps: 0

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QY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspPheArgCys 39
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DB 140 CACTGCACCAACCAAGAGACGAGTGTAGTGAAGGTGTAGGACGACGACTTCGGCTGCTGC 196
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RESULT 7
US-10-178-213-451
Sequence 451, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Canoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
TITLE OF INVENTION: Defensein Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 451
LENGTH: 461
TYPE: DNA
ORGANISM: Arachis hypogaea
FEATURE:
NAME/KEY: CDS
LOCATION: (44)...(271)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (128)...(268)
FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
; OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451

Alignment Scores:
Pred. No.: 5.94e-20 Length: 461
Score: 206.00 Matches: 33
Percent Similarity: 80.43% Conservative: 4
Best Local Similarity: 71.74% Mismatches: 7
Query Match: 74.91% Indels: 2
DB: 9 Gaps: 1

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Db 191 GACCACTGCAAGACAGACAGACACCTGCTCAGCGGCGCGCTGCCGCGACGATTTCCGCTGT 250
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QY 40 TrpCysThrLysArgCys 45
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RESULT 8
US-09-805-694B-5
; Sequence 5, Application US/09805694B
; Publication No. US20030041350A1
; GENERAL INFORMATION:
; APPLICANT: Kinney, Anthony
; TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
; FILE REFERENCE: B1432 US NA
; CURRENT APPLICATION NUMBER: US/09/805,694B
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,823
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (9)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
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; NAME/KEY: unsure
; LOCATION: (468)
; OTHER INFORMATION: n = A, C, G, or T
US-09-805-694B-5

Alignment Scores:
Pred. No.: 6.48e-20 Length: 494
Score: 206.00 Matches: 33
Percent Similarity: 78.72% Conservative: 4
Best Local Similarity: 70.21% Mismatches: 8
Query Match: 74.91% Indels: 2
DB: 9 Gaps: 1
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```
US-10-010-731-2 (1-45) x US-09-805-694B-5 (1-494)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18
   ::|||
Db 130 AAGACTTGCAGAACCTGGCTGATACATACAGGCTCCATGCTCCACTGCGACGCTGC 189
   ::|||

QY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
   |||
Db 190 GATGATCAGCTGCAAGACAAAGACACCTTCTCAGAGCGAGATGACAGGACGATTTTCGC 249
   |||

QY 39 CysTrpCysThrLysArgCys 45
   |||
Db 250 TGGTGACCCAGAAACTGT 270

RESULT 9
US-10-178-213-436
; Sequence 436, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Cyamopsis tetragonoloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(264)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (118)..(261)
US-10-178-213-436

Alignment Scores:
Pred. No.: 6.2e-20 Length: 420
Score: 205.50 Matches: 33
Percent Similarity: 79.17% Conservative: 5
Best Local Similarity: 68.75% Mismatches: 7
Query Match: 74.73% Indels: 3
DB: 9 Gaps: 1

US-10-010-731-2 (1-45) x US-10-178-213-436 (1-420)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 17
   ::|||
Db 118 AAGACATGTGAGATCTTGCAGATACATTCAGGCTCCATGCTCCCTGCAACGCCGACG 177
   ::|||

QY 18 CysAspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPhe 37
   |||
Db 178 TGCAGATGATCAGACAGACAAAGACACTTGTCTCAGCGAAGTGCAGACGATTTT 237
   |||

QY 38 ArgCysTrpCysThrLysArgCys 45
   |||
Db 238 CGCTGCTGTGTCACCAAAACTGT 261
   |||
```

```
RESULT 10
US-10-178-213-439
; Sequence 439, Application US/10178213
; Publication No. US20030041346A1
; GENERAL INFORMATION:
; APPLICANT: Slimmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensein Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Cymopsis tetragoloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(333)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (190)...(330)
US-10-178-213-439

Alignment Scores:
Pred. No.: 2,01e-19 Length: 563
Score: 203.00 Matches: 32
Percent Similarity: 80.85% Conservative: 6
Best Local Similarity: 68.09% Mismatches: 7
Query Match: 73.82% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-2 (1-45) x US-10-178-213-439 (1-563)

QY 1 ArgThcYgSLuAsnAlaAspLyTYrArgLYProCysPheSer-----GlyCys 18
      |||||||
Db 190 AGGACATGTGAGAGTGTGGACACATACAGGGGACCCGTTCACAGATGCTAGCTGC 249
      |||||||

QY 19 AspThHIScYstHrThrLYsgLuAsnAlaValSerGLYrGcYsArGAspAspPheArG 38
      |||||||
Db 250 GATGATCAGCTGCAGAGAACAGACCTTAATCATGAGTGAAGATGCAGAAATGATTTTCGC 309
      |||||||

QY 39 CystRpCysThrLYsArGcYs 45
      |||||||
Db 310 TGTGTGTCACCCAGAACTGT 330

RESULT 11
US-10-010-731-6
; Sequence 6, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Shah, Dilip
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
```

```
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT.193

TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear

FEATURE:
NAME/KEY: modified base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /mod_base= OTHER
/note="N" = A or C or G or T"

US-10-010-731-6

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Alignment Scores:
Pred. No.: 2.89e-17 Length: 293
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 67.27% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-2 (1-45) x US-10-010-731-6 (1-293)

QY 2 ThrCYsgLuAsnAlaAspLyTYrArgLYProCysPheSerGLYcYsAspThrHis 21
      |||||||
Db 176 ACTTGTGAGAGATTTGGCTAACATACAGGGGACCATGCTTCGCTGCTGCTTGCAC 235
      |||||||

QY 22 CystThrThrLYsgLuAsnAlaValSerGLYrGcYsArGAspAspPheArGcYs 39
      |||||||
Db 236 TGCMAAACCAAGAACACTTACTTACGCGNAGGTGCAGGAGACGACTTCGCTGC 289
      |||||||

RESULT 12
US-09-759-584-35
; Sequence 35, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P. A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
```

STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-759-584-35

Alignment Scores:
Pred. No.: 2.73e-15 Length: 141
Score: 168.00 Matches: 25
Percent Similarity: 70.21% Conservative: 8
Best Local Similarity: 53.19% Mismatches: 12
Query Match: 61.09% Indels: 2
DB: 10 Gaps: 1

US-10-010-731-2 (1-45) x US-09-759-584-35 (1-141)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTYrArgGlyProCysPhe-----SergIlyCys 18
|||
DB 1 AAGACTTGGAGACACTTCTGGAACCTTCAAGGACCATGATCCAGATGGAACATGC 60
|||
QY 19 AspThrHisCysThrThrylsGluAsnAlaValSerGlyArgCysArgspasPheArg 38
|||
DB 61 AACAAACATTTGCAAGAACACAGCATCTTCTTCTGGAAGATGACAGATGATTCNNN 120
|||
QY 39 CysTrpCysThrLysArgCys 45
|||
DB 121 TCGTGTGTCACCTAGAAACTGC 141
|||
RESULT 13
US-10-178-213-379
Sequence 379, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 379
LENGTH: 464
TYPE: DNA
ORGANISM: Cyamopsis tetragonoloba
FEATURE:
NAME/KEY: CDS
LOCATION: (32)...(256)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (116)...(253)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-379

Alignment Scores:
Pred. No.: 3.59e-13 Length: 464
Score: 157.50 Matches: 26
Percent Similarity: 68.09% Conservative: 6
Best Local Similarity: 55.32% Mismatches: 12
Query Match: 57.27% Indels: 3
DB: 9 Gaps: 2

US-10-010-731-2 (1-45) x US-10-178-213-379 (1-464)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTYrArgGlyProCysPhe-----GlyCys 18
|||
DB 116 AGAACATGTGAGAGTCCGCGACACATACAGGGGACCCGTTTCACTGAGGGTACTGC 175
|||
QY 19 AspThrHisCysThrThrylsGluAsnAlaValSerGlyArgCysArgspasPheArg 38
|||
DB 176 GATGATCATTTGCAAGAACACAGCATCTTATCATGATGTAACATGCAAA---CAGTTAGCC 232
|||
QY 39 CysTrpCysThrLysArgCys 45
|||
DB 233 TCGTGTGTCACCTAGAAACTGT 253
|||
RESULT 14
US-10-178-213-37
Sequence 37, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 635
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: CDS
LOCATION: (149)...(403)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2003, 06:14:34 ; Search time 1048.24 Seconds

(without alignments)
695.261 Million cell updates/sec

Title: US-10-010-731-2

Perfect score: 275

Sequence: 1 RTCENLADKXRGPCFSGCDT.....ENAVSGRCRDPFCWCTKRC 45

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh

-O/cp2_1/uspro.spool/us10010731/runat_17062003_095705_28177/app_query.fasta.1.398

-DB-EST -OPMT=fastcap -SUFFIX=ist -MINMATCH=0.1 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=DIOSum62 -TRANS=human40.cdi -LIST=45

-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

-USR=us10010731.ecgn.1.1.2463 @runat.17062003.095705.28171 -NCPU=6 -ICPU=3

-NMR=MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlu:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estlom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vtc:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	97.1	446	9	AJ498901
2	197	71.6	487	13	B1321179
3	172	62.2	426	12	BG838678
4	171	62.5	517	9	AJ308155
5	154.5	56.2	574	14	BO151477
6	141.5	51.5	503	12	BF633403
7	136	49.5	366	13	B1321308
8	116	42.2	438	13	B1642738
9	108	39.3	442	13	BM110496
10	104	37.8	187	12	BF598147
11	104	37.8	292	10	AM203222
12	104	37.8	400	14	BO249330
13	104	37.8	485	13	B1299919
14	104	37.8	492	13	BJ298033
15	104	37.8	502	12	BG838277
16	104	37.8	506	12	BG838599
17	104	37.8	522	13	BJ296553
18	104	37.8	528	12	BG838299
19	104	37.8	526	13	BJ293856
20	104	37.8	566	13	BJ290214
21	103	37.5	212	10	BE611505
22	103	37.5	238	12	BG238242
23	103	37.5	259	12	BG405833
24	103	37.5	295	13	B1469191
25	103	37.5	300	13	B1972271
26	103	37.5	314	10	BE611109
27	103	37.5	323	9	A1495809
28	103	37.5	336	13	B1787994
29	103	37.5	356	12	BE805922
30	103	37.5	356	12	BE805922
31	103	37.5	359	9	A1441508
32	103	37.5	364	10	AW336579
33	103	37.5	364	13	B1788286
34	103	37.5	376	10	AW734140
35	103	37.5	378	10	AW733894
36	103	37.5	390	13	B1972041
37	103	37.5	393	13	BM143218
38	103	37.5	400	9	A1938187
39	103	37.5	403	12	BG041846
40	103	37.5	407	14	BQ081406
41	103	37.5	409	13	B1972131
42	103	37.5	420	13	B1971605
43	103	37.5	420	14	BM954394
44	103	37.5	420	14	BQ080027
45	103	37.5	420	14	BQ080612

ALIGNMENTS

RESULT 1
AJ498901
LOCUS
DEFINITION AJ498901 MTP0SE Medicago truncatula cDNA clone mt-acc955209h10,
ACCESSION AJ498901
VERSION AJ498901.1 GI:22089344
KEYWORDS
SOURCE
ORGANISM
barrel medic.
Medicago truncatula
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Rosidae: eurosids II: Fabales: Fabaceae: Papilionoideae: Trifoliaceae:
Medicago.
REFERENCE
1 (bases 1 to 446)

AUTHORS	Firnhaber,C., Bartelsmeyer,V., Meyer,F., Bartels,D., Bekel,T., Linke,B., Puchler,A. and Kuester,H. Determination of transcript sequences from developing pods including seeds of Medicago truncatula genotype A17 unpublished (2002)
JOURNAL	Contact: Kuester H
COMMENT	Lehrstuhl fuer Genetik Universitaet Bielefeld Postfach 100131, D-33501 Bielefeld, Germany.
FEATURES	Location/Qualifiers
source	1. 446
	/organism="Medicago truncatula"
	/db_xref="taxon:3880"
	/clone="mt--acc95209h10"
	/clone_lib="MTPOSE"
	/tissue_type="pods including seeds"
	/dev_stage="different stages of development"
	/note="vector: pGEM-T; Site.1: PstI; Site.2: SphI; genotype A17: cDNA was prepared from polyA+ enriched RNA from developing pods including seeds harvested at different stages of development. The cDNA was directionally ligated by Medigenomix into the pGEM-T vector from Promega using GCATCGGCGCGGCGGCACATG and CTCGAGCCATTATGGCCGGG adapters. Plasmids containing cDNA inserts were propagated in E. coli DH10B cells."
BASE COUNT	147 a 84 c 83 g 132 t
ORIGIN	
Alignment Scores:	
Pred. No.:	3.5e-24 Length: 446
Score:	267.00 Matches: 43
Percent Similarity:	97.78% Conservative: 1
Best Local Similarity:	95.36% Mismatches: 1
Query Match:	97.09% Indels: 0
DB:	9 Gaps: 0
US-10-010-731-2 (1-45) x AJ498901 (1-446)	
OY	1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
Db	142 AAGACTGTGTGAAGATTTCGTGATTAATACAGGGAGCACCATGCTTAGTGTTGATPACT 201
OY	21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysAspAspPheArgCysTrp 40
Db	202 CACATGCATACCACAAAGAGAATGCAGTTAGCGGACAGTGCAGGAGATCTTCGTGTGG 261
OY	41 CysThrLysArgCys 45
Db	262 TGTACTAAAACTGT 276
RESULT 2	
LOCUS	B1321179 487 bp mRNA linear EST 29-NOV-2001
DEFINITION	saf48610.y3 Gm-cl077 glycine max cDNA clone GENOME SYSTEMS CLONE
VERSION	B1321179.1 GI:15000365
KEYWORDS	EST.
ORGANISM	soybean.
REFERENCE	1 (bases 1 to 487)
AUTHORS	Shoemaker,R., Kelm,P., Vodkin,L., Eipelting,J., Coryell,V., Khanna
	,A., Bolla,B., Marita,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.C.,
	Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
	,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
	,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
	,R., Waterston,R. and Wilson,R.
TITLE	Public Soybean EST Project

```

JOURNAL
COMMENT
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Putative full length read
vector to vector length is this clone is available through: ResGen,
Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801
For further information call: (800)-533-4363 or contact via email:
csh@resgen.com
Seq primer: ~40RP from Gibco
High quality sequence stop: 432.
Location/Qualifiers
1. .487
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1077-1723"
/clone_id="Gm-c1077"
/tissue_type="18 day old 'Williams' seedlings"
/dev_stage="18 day old 'Williams' seedlings"
/lab_host="DH10B"
/note="vector: pBluescript II SK+, Site_1: EcoRI; Site_2:
XhoI; The mRNA was isolated from cotyledons of 18-day-old
'Williams' seedlings which were greenhouse grown in
potting soil. The cotyledons were flash-frozen in liquid
nitrogen. StrataGene's cDNA Synthesis Kit (catalog number
200401) was used to synthesize the cDNA. First-strand
synthesis was performed with 5-methyl dCTP, hence the
ligated cDNA was hemimethylated. A modification of
StrataGene's first-strand synthesis primer was used. An
'anchor' nucleotide (V-A, C, or G) was added to the 3' end
of the primer [GAGAGAGAGAGAGAGACACTGCTGAG(T)18V] to
anchor the primer at the 5' end of the poly(A) tract.
After second-strand synthesis, the cDNA ends were filled
in with cloned Pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The cDNA was then
precipitated and redissolved in sterile, RNase-
free water. The XhoI site within the first- strand
synthesis primer was then restricted by digestion with
XhoI from Promega (40U/ul); all XhoI sites in the cDNA
would be protected by their hemimethylated status. The
cDNA constructs were size-fractionated with a 500bp
cutoff, using Sephacryl S-500 High Resolution (Pharmacia
Biotech) in a 2-mm diameter column and a bed volume of
approximately 1ml. The column eluent was precipitated,
redissolved, and ligated into StrataGene's pBluescript II
XR predigested vector (pBluescript II SK(+)) vector that
has been digested with EcoRI and XhoI, and phosphorylated
by StrataGene). This library was constructed in the
laboratory of Dr. Paul Keim and Dr. Virginia H. Corryell at
Northern Arizona University."
BASE COUNT
152 a 96 c 102 g 137 t
ORIGIN
Alignment Scores:
3.13e-15 Length: 487
Pred. No.: 197.00 Matches: 42
Score: 76.608 Conservative: 4
Percent Similarity: 68.09% Mismatches: 9
Best Local Similarity: 71.64% Indels: 2
Query Match: 13 Gaps: 1
DB: 13
US-10-010-731-2 (1-45) x B1321179 (1-487)
1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 111
Db 152 AAGACTTGCGAGAACCGTCGATACATACAGGGGCTCATCTTCACACACATGCGACGCGC 211
19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysAlaGAspAspPheArg 38
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 111

```

Db 212 GATGATTTCGACAGACAAAGACACTTGTCTCAGAGGCGATGACGATTTTCCG 271
QY 39 CystPCysThrLysArgCys 45
|||||
Db 272 TGTGTGTCACCAAAACTGT 292

RESULT 3
BG838678/c 426 bp mRNA linear EST 25-MAY-2001
LOCUS BG838678/c
DEFINITION glycine clandestina cDNA clone Gc01_03f01, mRNA sequence.
ACCESSION BG838678
VERSION BG838678.1 GI:14204985
KEYWORDS EST.
SOURCE glycine clandestina.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 426)
Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Glycine clandestina Seedlings
JOURNAL Unpublished (2001)
COMMENT Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.

FEATURES
source location/Qualifiers
1..426
/organism="Glycine clandestina"
/cultivar="1035"
/db_xref="taxon:45687"
/clone="Gc01_03f01"
/clone_1lb="Gc01_AMFC_ECORC_cold_stressed_Glycine_clandestina"
/tissue_type="Leaves, stem"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Plants incubated at 2 degrees under 12 hours of light/day. Harvested after only 2-5 days of cold treatment. cDNA was prepared with the Uni-Zap cDNA kit from Stratagene. Eco RI adapters were linked followed by digest with Xho I/Eco RI and ligated to pBluescript."

BASE COUNT 116 a 92 c 86 g 125 t 7 others
ORIGIN

Alignment Scores:
Pred. No.: 3..92e-12 Length: 426
Score: 172.00 Matches: 29
Percent Similarity: 73.91% Conservative: 5
Best Local Similarity: 63.04% Mismatches: 10
Query Match: 62.55% Indels: 2
DB: 12 Gaps: 1

US-10-010-731-2 (1-45) x BG838678 (1-426)

QY 2 ThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCysAsp 19
|||||
Db 316 ACTTGGAGAACTGGCTATATACATCAGGGGTCACGTCTACCTACCGGACCTCGCAT 257
|||||

QY 20 ThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39
|||||
Db 256 GATCACTGCAGAAAGATTAAGAACTTACTACGCGGCGAGGTGACGACVATTTTCGCTGH 197
|||||

QY 40 TrpCysThrLysArgCys 45
|||||

Db 196 TGGHGCACGCAAAACTGT 179
RESULT 4
AJ308155 517 bp mRNA linear EST 29-OCT-2001
LOCUS AJ308155
DEFINITION AJ308155 SSH Pisum sativum cDNA clone PSSSH1clone91, mRNA sequence.
ACCESSION AJ308155
VERSION AJ308155.1 GI:16507870
KEYWORDS EST.
SOURCE pea.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

REFERENCE 1 (bases 1 to 517)
Grunwald,U., Lapopin,L., Becker,A., Mann,P., Bomanski,K.N., Gianinazzi-Pearson,V. and Franken,P.
Screening for genes activated in Pisum sativum mycorrhiza by arbuscule development-related expression profiling
JOURNAL Unpublished (2001)
COMMENT Contact: Franken P
Biochemistry
Max-Planck-Institute for Terrestrial Microbiology
Marburg, Karl-von-Frisch-Strasse, D-35043, Germany.
location/Qualifiers
1..517
/organism="Pisum sativum"
/cultivar="Finale"
/db_xref="taxon:3888"
/clone="PSSSH1clone91"
/clone_1lb="SSH"
/tissue_type="arbuscular mycorrhiza"
/note="minus inoculated late mutant"

BASE COUNT 161 a 87 c 102 g 167 t
ORIGIN

Alignment Scores:
Pred. No.: 6..86e-12 Length: 517
Score: 171.00 Matches: 26
Percent Similarity: 70.21% Conservative: 7
Best Local Similarity: 55.32% Mismatches: 12
Query Match: 62.18% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-2 (1-45) x AJ308155 (1-517)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18
:::|||||
Db 159 AAAACTGTGAGATTTGTTGGCACATTCAGAGGACCATCCAGATGTAATCTGC 218
:::|||||

QY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
:::|||||
Db 219 AACAAACATTGCGAGGAACCAAGCACTTACTAGTGGAGGTGCAAGGATGATTTTCCG 278
:::|||||

QY 39 CystPCysThrLysArgCys 45
|||||
Db 279 TGTGTGTCACCTCGAAACTGT 299
|||||

RESULT 5
BO151477 574 bp mRNA linear EST 24-APR-2002
LOCUS BO151477
DEFINITION NF088A06.F1038 Developing leaf Medicago truncatula cDNA clone.
ACCESSION BO151477
VERSION BO151477.1 GI:2028536
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 574)
AUTHORS Flores-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W., and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula leaf library
COMMENT Unpublished (2000)
CONTACT: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 574 Std Error: 0.00
Plate: 088 row: A column: 06
Seq primer: TCACACAGCAACACGCTATGAC.
Location/Qualifiers
FEATURES
Source
1..574
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_11b="NF088A06Lr"
/clone_11b="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
BASE COUNT 198 a 104 c 104 g 167 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 9.93e-10 Length: 574
Score: 154.50 Matches: 26
Percent Similarity: 72.34% Conservative: 8
Best Local Similarity: 55.32% Mismatches: 10
Query Match: 56.18% Indels: 3
DB: 14 Gaps: 2
US-10-010-731-2 (1-45) x BQ151477 (1-574)
QY 1 ArgThhCysGluAsnAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18
|||||
DB 140 AGCACTTGATGAGCATTTGGCTGATACATACAGAGGACATGCTTCACGAGAGTACTGT 199
19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
|||||
DB 200 GATGACCACTGCAAGAAACAAGACACTTATATAGTGGCAGCGGCCAT---AACTTCA 256
39 CysTTPCysThrLysArgCys 45
|||||
DB 257 TGTTCCTGCACCTCAAAACTGT 277
RESULT 6
BF633403 503 bp mRNA linear EST 19-DEC-2000
LOCUS NF047E03DTJF1022 Drought Medicago truncatula cDNA clone NF047E03DT
DEFINITION 5', mRNA sequence.
ACCESSION BF633403
VERSION BF633403.1 GI:11897561
KEYWORDS EST.
SOURCE
ORGANISM
Medicago truncatula
barel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 503)
REFERENCE
AUTHORS Flores-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W., and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula drought library
COMMENT Unpublished (2000)
CONTACT: May GD
Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 503 Std Error: 0.00
Plate: 047 row: E column: 03
Seq primer: TCACACAGCAACACGCTATGAC.
Location/Qualifiers
FEATURES
Source
1..503
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF047E03DT"
/clone_11b="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."
BASE COUNT 181 a 82 c 93 g 147 t
ORIGIN
Alignment Scores:
Pred. No.: 3.72e-08 Length: 503
Score: 141.50 Matches: 26
Percent Similarity: 70.83% Conservative: 8
Best Local Similarity: 54.17% Mismatches: 10
Query Match: 51.45% Indels: 4
DB: 12 Gaps: 2
US-10-010-731-2 (1-45) x BF633403 (1-503)
QY 1 ArgThhCysGluAsnAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18
|||||
DB 146 AGCACTTGATGAGCATTTGGCTGATACATACAGAGGACCATGCTTCACGAGAGTACTGT 205
19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
|||||
DB 206 GATGACCACTGCAAGAAACAAGACACTTATATAGTGGCAGCGGCCAT---AACTTCA 262
38 gCysTTPCysThrLysArgCys 45
|||||
DB 263 ATGTTCTGCACCTCAAAACTGT 284
RESULT 7
BI321308 366 bp mRNA linear EST 29-NOV-2001
LOCUS BI321308
DEFINITION 366 bp mRNA linear EST 29-NOV-2001
ID: Gm-cl077-2037 5' similar to SW:10KD_YIGUN P18646 10 KD PROTEIN
PRECUSOR ;, mRNA sequence.
ACCESSION BI321308
VERSION BI321308
KEYWORDS EST.
SOURCE
ORGANISM
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 366)
REFERENCE
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck
R., Ritters, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
CONTACT: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Hunttsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccure@resgen.com
Seq. primer: -40RP from Gldco
high quality sequence, stop: 343.

BASE COUNT ORIGIN	124 a	60 c	70 g	112 t
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VERSION	BI642738.1	GI:15544948
KEYWORDS	EST.	
SOURCE	Robinia pseudoacacia.	
ORGANISM	Robinia pseudoacacia	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
	Rosidae; eustosids I; Finales; Fabaceae; Papilionoideae; Robinieae;	
	Robiniinae.	
REFERENCE	1 (bases 1 to 438)	
AUTHORS	Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Retzel, E.F.,	
	Kemdem, D.P. and Keathley, D.E.	
TITLE	Analysis of gene expression patterns in trunk wood of a mature	
	black locust (Robinia pseudoacacia)	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Kyung-Hwan Han	
	Department of Forestry	
	Michigan State University	
	126 Natural Resources, East Lansing, MI 48824-1222, USA	
	Tel: 517 353 4751	
	Fax: 517 432 1143	
	Email: hanky@msu.edu.	
FEATURES	Location/Qualifiers	
SOURCE	1..438	

BASE COUNT	134 a	80 c	86 g	124 t	14 others
ORIGIN					

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
1 (bases 1 to 292)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccorresgen.com
Insert Length: 578 Std Error: 0.00
High quality sequence stop: 280.
Location/Qualifiers

FEATURES

Source

1..292
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-1211"
/clone_1lb="Gm-cl028"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
/note="Vector: pBluescript II XR. Site_1: EcoRI. Site_2: XhoI. The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicus, strain USDA110 prior to harvest. StrataGene's cDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dcrp, hence the ligated cDNA was hemimethylated. A modification of StrataGene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A-C, or G) was added to the 3' end of the primer (GAGACGAGACGAGACGAGACGAG(T)18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GIBCOBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into StrataGene's pBluescript II XR predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by StrataGene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Corryell."

BASE COUNT
ORIGIN
66 a 68 c 68 g 89 t 1 others

Alignment Scores:

Pred. No.: 292
Score: 104.00
Percent Similarity: 59.18%
Best Local Similarity: 44.90%
Query Match: 37.82%
DB: 10
Length: 292
Matches: 22
Conservative: 7
Mismatch: 14
Indels: 6
Gaps: 4

US-10-010-731-2 (1-45) x AW203222 (1-292)

Oy 1 ArgthrcysguasnlauaAsplysTyArgGlyProcysPheSer-----GlyCys 18
|||||
Db 119 AGAACTGTGAGTCTCAAGCCACCTTTCAAGGGCCATGTTGAGTGCACCACTGT 178
::: |||
Oy 19 AspThrcysGthrThrlysgluasnlauaValserGlyArGysArGAspAspPheArg 38
::: |||
Db 179 GGCTGCTTTGGCCGACAC---GAAAGCTTCACTGAGGACACATCGCT---GGCTTCGCT 232
39 -----CysTrpCysThrlyArGys 45
|||
Db 233 CGCAAAATGCTTGTGACCAACAACTGT 259

RESULT 12
LOCUS B0249330
DEFINITION TAE23045B10R TAE25 Triticum aestivum cDNA clone TAE23045B10R, mRNA sequence.
ACCESSION B0249330
VERSION B0249330.1 GI:20445206
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 400)
Location/Qualifiers

REFERENCE
AUTHORS Cloutier, S.
TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL Unpublished (2002).
COMMENT Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-Food Canada
195 Dfoe Rd. Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
This clone was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >870 bp
plate: 045 row: B column: 10
Seq primer: M13 Reverse.

FEATURES

Source

1..400
/organism="Triticum aestivum"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TAE23045B10R"
/clone_1lb="TAE25"
/tissue_type="developing seeds"
/dev_stage="25 days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies); Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 25 days post-anthesis"

BASE COUNT
ORIGIN
85 a 123 c 121 g 71 t

Alignment Scores:

Pred. No.: 400
Score: 104.00
Percent Similarity: 60.00%
Best Local Similarity: 42.00%
Query Match: 37.82%
DB: 14
Length: 400
Matches: 21
Conservative: 9
Mismatch: 14
Indels: 6
Gaps: 3

US-10-010-731-2 (1-45) x B0249330 (1-400)

Oy 1 ArgthrcysguasnlauaAsplysTyArgGlyProcysPhe-----SerGlyCys 18
|||||
Db 181 CGGACGTGCGAGTGCAGACCAAGTTCAAGGCCCCCTCTTCAGCGACCACTGC 240
|||
Oy 19 AspThrcysGthrThrlysgluasnlauaValserGlyArGysArGAsp----- 35
|||

Db 241 GCACCGTGTGCCGACC---GAGAACTTTCCCGCGGCGCAGTGCACACGACACGCTC 297

Qy 36 AsphearGcYstrpCysThrLysArgCys 45
Db 298 GAGCGCAAGTGTCTACTGCGAGCGGACTGC 327

RESULT 13

LOCUS Bt299919/c 485 bp mRNA linear EST 09-Apr-2002

DEFINITION Bt299919 Y. Ogihara unpublished cDNA library, Wh_SL Triticum aestivum cDNA clone whsl32117 3', mRNA sequence.

ACCESSION Bt299919

VERSION Bt299919.1 GI:20111909

KEYWORDS EST.

SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 485)
AUTHORS Ogihara,Y. and Murai,K.
TITLE Expressed genes in Triticum aestivum
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
Source Location/Qualifiers
1..485
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whsl32117"
/rname="whsl32117"
/rsize="485"
/rstage="Feekes" scale 11.3"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site.1: EcoRI; Site.2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J. Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T3 Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 99 a 143 c 139 g 102 t 2 others

ORIGIN

Alignment Scores:
Pred. No.: 0.00207 Length: 485
Score: 104.00 Matches: 21
Percent Similarity: 60.00% Conservative: 9
Best Local Similarity: 42.00% Mismatches: 14
Query Match: 37.82% Indels: 6
DB: 13 Gaps: 3

US-10-010-731-2 (1-45) x Bt299919 (1-485)

Qy 1 ArghrhcysgluasnleuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18
Db 318 CGGACGTGCGAGTGTGCAGAGCCACAGTTCAAGGCGCCCTGCTTCAGCGACGACCACTGC 259

Qy 19 AsphrhtscysThrThrLysGluAsnAlaValSerGlyArgCysArgAsp----- 35
Db 258 GCACACCGTGTGCCGACC---GAGAACTTTCCCGCGGCGCAGTGCACACGACGACGCTC 202

Qy 36 AsphearGcYstrpCysThrLysArgCys 45
Db 201 GAGCGCAAGTGTCTACTGCGAGCGGACTGC 172

RESULT 14

LOCUS Bt298033/c 492 bp mRNA linear EST 09-Apr-2002

DEFINITION Bt298033 Y. Ogihara unpublished cDNA library, Wh_SL Triticum aestivum cDNA clone whsl23b04 3', mRNA sequence.

ACCESSION Bt298033

VERSION Bt298033.1 GI:20111065

KEYWORDS EST.

SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 492)
AUTHORS Ogihara,Y. and Murai,K.
TITLE Expressed genes in Triticum aestivum
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
Source Location/Qualifiers
1..492
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whsl23b04"
/rname="whsl23b04"
/rsize="492"
/rstage="Feekes" scale 11.3"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site.1: EcoRI; Site.2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J. Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T3 Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 102 a 143 c 141 g 106 t

ORIGIN

Alignment Scores:
Pred. No.: 0.00211 Length: 492
Score: 104.00 Matches: 21
Percent Similarity: 60.00% Conservative: 9
Best Local Similarity: 42.00% Mismatches: 14
Query Match: 37.82% Indels: 6
DB: 13 Gaps: 3

US-10-010-731-2 (1-45) x Bt298033 (1-492)

Qy 1 ArghrhcysgluasnleuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18
Db 329 CGGACGTGCGAGTGTGCAGAGCCACAGTTCAAGGCGCCCTGCTTCAGCGACGACCACTGC 270

Qy 19 AsphrhtscysThrThrLysGluAsnAlaValSerGlyArgCysArgAsp----- 35
Db 269 GCACACCGTGTGCCGACC---GAGAACTTTCCCGCGGCGCAGTGCACACGACGACGCTC 213

Qy 36 AsphearGcYstrpCysThrLysArgCys 45
Db 269 GCACACCGTGTGCCGACC---GAGAACTTTCCCGCGGCGCAGTGCACACGACGACGCTC 213

DB 212 GAGCGCAGTGCTACTGCGAGCGGACTGC 183

Job time : 1052.24 secs

RESULT 15
BG838277

LOCUS

DEFINITION

502 bp mRNA

linear EST 25-MAY-2001

Gc01_10f03_R Gc01_AAFc_ECORC_cold_stressed_glycine_clandestina

glycine clandestina

CDNA clone Gc01_10f03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine clandestina.

Glycine clandestina

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine

1 (bases 1 to 502)

Singh,J.A., Farah,S., Chapados,J., Courroux,P., De Moors,A., Harris

,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker

,N.A.

Expressed Sequence Tags from Cold-Stressed Glycine clandestina

Seedlings

Unpublished (2001)

Contact: Singh,J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A

0C6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singhja@em.agr.ca.

Location/Qualifiers

1.502

/organism="Glycine clandestina"

/cultivar="1035"

/db_xref="taxon:45687"

/clone="Gc01_10f03"

/clone_1lb="Gc01_AAFc_ECORC_cold_stressed_glycine_clandest

ina"

/tissue_type="leaves, stem"

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;

Site_2: XhoI; Plants incubated at 2 degrees under 12 hours

of light/day. Harvested after only 2-3 days of cold

treatment. cDNA was prepared with the Uni-Zap cDNA kit

from Stratagene. Eco RI adapters were linked followed by

digest with Xho I/Eco RI and ligated to p Bluescript."

BASE COUNT 123 a 93 c 105 g 179 t 2 others

ORIGIN

Alignment Scores:

Pred. No.: 0.00217

Score: 104.00

Percent Similarity: 61.228

Best Local Similarity: 42.868

Query Match: 37.828

DB: 12

Gaps: 3

US-10-010-731-2 (1-45) x BG838277 (1-502)

QY 1 ArgTthCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20

|||||

DB 104 AGAAGTTGTGAGCTCAGAGCCACCGTTTCAGAGGGCGCATGTGAGT-----GACACC 157

QY 21 HisCysThr-----LysGluAsnAlaValSerGlyArgCysArgAsp---Asp 36

|||||

DB 158 AACTGTGCTCTGTTCATACCGAAGTTTCATCGAGAGACAATGCCGTGGCTTGCCT 217

QY 37 PheArgCysTrpCysThrLysArgCys 45

|||||

DB 218 CGAGATGCTCTGCACCAACAATGTGT 244

Search completed: June 21, 2003, 07:52:30

~~BEST AVAILABLE COPY~~

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 04:45:23 ; Search time 150 Seconds
(without alignments)
3753.331 Million cell updates/sec

Title: US-10-010-731-13

Perfect score: 250
Sequence: 1 GGGGATCCCAATCTAATCA.....AAAGATGTAAGATCCCC 250

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	250	100.0	250	19	AAV39187	Alfalfa plant anti
2	234	93.6	507	19	AAV39195	Antifungal polypep
3	232.4	93.0	490	19	AAV39186	Antifungal polypep
4	179.8	93.0	200	19	AAV39190	Antifungal polypep
5	169.6	67.8	293	19	AAV39191	Antifungal polypep
6	156.4	62.6	468	21	AAZ49412	Pea Defensin prote
7	119.4	47.8	494	22	AAAD17530	Soybean Gly m2 pro
8	117.8	47.1	327	19	AAV39194	Antifungal polypep
9	62	24.8	62	19	AAV39196	Antifungal polypep

C	10	47	18.8	47	19	AAV39197	Antifungal polypep
	11	40.6	16.2	217	21	AAZ94226	Antifungal protein
	12	40	16.0	141	15	AAO70126	Antimicrobial Lc-A
C	13	35.2	14.1	9542	20	AAV20260	Borrelia burgdorfe
	14	32.2	12.9	138	14	AAO38648	Encodes antifungal
	15	32.2	12.9	505	23	ABV12096	Human prostate exp
	16	32.2	12.9	12138	24	ABL33942	Human immune syste
	17	32.2	12.9	12138	24	ABK28335	DNA transcription
	18	31.6	12.6	1809	23	AAV81268	DNA encoding novel
	19	31.4	12.6	56583	21	AAV21125	Human low adenosin
	20	31.4	12.6	56583	21	AAA35003	Human adenosine re
	21	31.4	12.6	910715	20	AAV20248	Borrelia burgdorfe
C	22	31.2	12.5	37948	20	AAZ06831	Photorehabus lunn
	23	30.8	12.3	653	22	AAH97918	Murine 7-transmem
C	24	30.8	12.3	1563	22	AAH64828	Human secreted pro
	25	30.6	12.2	487	21	AAV38169	Arabidopsis thalia
C	26	30.6	12.2	487	24	ABK30864	Plant dwarfing/stu
	27	30.6	12.2	502	24	ABK45283	CDNA encoding colo
C	28	30.6	12.2	620	24	ABO66218	Arabidopsis thalia
	29	30.6	12.2	709	24	ABK30321	Human G-protein-co
C	30	30.6	12.2	1094	24	ABL49499	Sequence #101 used
	31	30.6	12.2	1094	24	ABK30690	Plant dwarfing/stu
	32	30.6	12.2	1636	21	AAV58012	1636 bp Candida al
	33	30.6	12.2	1712	21	AAV57960	Human prostate exp
	34	30.6	12.2	2435	23	ABV22550	Human prostate exp
	35	30.6	12.2	2435	23	ABV25004	Human prostate exp
	36	30.6	12.2	2435	23	ABV25302	Human prostate exp
	37	30.6	12.2	2435	23	ABV28367	Human prostate exp
	38	30.6	12.2	3058	22	AAH33402	Human colon cancer
	39	30.4	12.2	1140	20	AAV58881	Human FAK-related
	40	30.4	12.2	3791	22	AAV65534	Human focal adhesi
	41	30.4	12.2	3791	22	AAV15382	Human focal adhesi
	42	30.4	12.2	4052	23	ABV29192	Human prostate exp
C	43	30.4	12.2	4481	24	AAV94837	Human DNA sequence
	44	30.2	12.1	1036	24	ABK35277	Human CDNA encodi
C	45	30.2	12.1	1122	22	AAV64478	beta-lactamase 11

ALIGNMENTS

RESULT 1	
ID	AAV39187 standard; DNA; 250 BP.
AAV39187	
XX	AAV39187;
AC	
XX	
DT	25-SEP-1998 (first entry)
XX	
DE	Alfalfa plant antifungal polypeptide ALFALF1 encoding DNA.
XX	
KW	Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW	plant pathogenic fungus; Alfafp1; Alfafp2; ds.
XX	
OS	Medicago sativa.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS
FT	/*tag= a
FT	/product= "mature ALFALF1"
PN	W09826083-AL.
XX	
PD	18-JUN-1998.
XX	
PF	11-DEC-1997; 97WO-US22662.
XX	
PR	13-DEC-1996; 96US-0766355.
XX	
PA	(MONS) MONSANTO CO.
XX	
PI	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;

DR WPI; 1998-348537/30.
 XX P-PSDB; AAW61964.
 XX Antifungal poly(peptide)s and genes isolated from alfalfa plant(s)
 PT - used to control plant pathogenic fungi and to produce transformed
 PT plants with increased fungal resistance
 XX
 XX Claim 3; Page 78; 97pp: English.
 XX This DNA encodes an antifungal polypeptide, AlfAP1 isolated from
 CC alfalfa plants (Medicago). The polypeptides AlfAP1 and AlfAP2 are
 CC useful to control plant fungi, especially pathogenic fungi, by
 CC transforming plant cells with a vector comprising sequences encoding
 CC AlfAP1 or AlfAP2 to allow expression of antifungally effective amounts
 CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
 CC cotton and especially potato. Micro-organisms may also be transformed
 CC to produce the polypeptides, and applied to plants to control plant
 CC fungi. The polypeptides can also be included with a suitable solvent in
 CC antifungal compositions and these can be administered to plants to
 CC control plant fungi. Such compositions and genetically engineered plants
 CC may also contain additional molecules e.g. the compositions can contain
 CC other antifungal agents or the plants contain DNA encoding insecticidal
 CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
 CC to prepare antibodies useful to detect polypeptides or isolate other
 CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
 CC to produce polypeptides and transgenic plants and as probes or primers in
 CC nucleic acid hybridisation e.g. to detect complementary sequences in
 CC samples, and to prepare mutants or isolate similar sequences from related
 CC species.
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 S0 Sequence 250 BP; 73 A; 48 C; 64 G; 65 T; 0 other:
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 Best local similarity 100.0%; Pred. No. 3.1e-73;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGATCCCAATCTAATCAACTATGAGAGAGAAATCACTAGCTGCTTATGCTTCTCT 60
 DB 1 GGGGATCCCAATCTAATCAACTATGAGAGAGAAATCACTAGCTGCTTATGCTTCTCT 60
 QY 61 TCTTGCTCTCTTGTGACAAAGAAATGCTGACAGAGCAACATGAGCAAT 120
 DB 61 TCTTGCTCTCTTGTGACAAAGAAATGCTGACAGAGCAACATGAGCAAT 120
 QY 121 TGGCAGATTAATATAGGGAGCAGCTTATGCTGACACTCACTGACAAACCAAG 180
 DB 121 TGGCAGATTAATATAGGGAGCAGCTTATGCTGACACTCACTGACAAACCAAG 180
 QY 181 AGACGCACTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGTACTAAAGATGTT 240
 DB 181 AGACGCACTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGTACTAAAGATGTT 240
 QY 241 AAGGATCCCC 250
 DB 241 AAGGATCCCC 250
 RESULT 2
 ID AAV39195 standard; DNA; 507 BP.
 XX AAV39195;
 XX 25-SEP-1998 (first entry)
 XX Antifungal polypeptide AlfAP1 mature sequence encoding DNA.
 DE Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
 KW plant pathogenic fungus; AlfAP1; AlfAP2; ds.
 XX Medicago sativa.
 OS
 XX
 FH Key Location/Qualifiers

FT CDS 173..310
 FT /*tag= a
 FT /product= "mature AlfAP1"
 XX WO9826083-A1.
 XX .18-JUN-1998.
 XX
 XX 11-DEC-1997; 97MO-US22662.
 XX
 XX .13-DEC-1996; 96US-0766355.
 XX (MONS) MONSANTO CO.
 XX
 XX Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
 DR WPI; 1998-348537/30.
 DR P-PSDB; AAW61964.
 XX
 XX Antifungal poly(peptide)s and genes isolated from alfalfa plant(s)
 PT - used to control plant pathogenic fungi and to produce transformed
 PT plants with increased fungal resistance
 XX
 XX Claim 5; Page 77; 97pp: English.
 XX This DNA encodes an antifungal polypeptide, AlfAP1 isolated from
 CC alfalfa plants (Medicago). The polypeptides AlfAP1 and AlfAP2 are
 CC useful to control plant fungi, especially pathogenic fungi, by
 CC transforming plant cells with a vector comprising sequences encoding
 CC AlfAP1 or AlfAP2 to allow expression of antifungally effective amounts
 CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
 CC cotton and especially potato. Micro-organisms may also be transformed
 CC to produce the polypeptides, and applied to plants to control plant
 CC fungi. The polypeptides can also be included with a suitable solvent in
 CC antifungal compositions and these can be administered to plants to
 CC control plant fungi. Such compositions and genetically engineered plants
 CC may also contain additional molecules e.g. the compositions can contain
 CC other antifungal agents or the plants contain DNA encoding insecticidal
 CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
 CC to prepare antibodies useful to detect polypeptides or isolate other
 CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
 CC to produce polypeptides and transgenic plants and as probes or primers in
 CC nucleic acid hybridisation e.g. to detect complementary sequences in
 CC samples, and to prepare mutants or isolate similar sequences from related
 CC species.
 XX
 S0 Sequence 507 BP; 181 A; 85 C; 102 G; 136 T; 3 other:
 Query Match 93.6%; Score 234; DB 19; Length 507;
 Best local similarity 100.0%; Pred. No. 8.9e-68;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 CAATCTAATCAACTATGAGAGAAATCACTAGCTGCTTATGCTTCTCTTCTGTT 68
 DB 77 CAATCTAATCAACTATGAGAGAAATCACTAGCTGCTTATGCTTCTCTTCTGTT 136
 QY 69 CTCCTTGTGACAAAGAAATGCTGACAGAGCAACATGAGCAATTTGGCAGAT 128
 DB 137 CTCCTTGTGACAAAGAAATGCTGACAGAGCAACATGAGCAATTTGGCAGAT 196
 QY 129 AATATAGGGAGCAGCTTATGCTGACACTCACTGACCAACCAAGAGACGA 188
 DB 197 AATATAGGGAGCAGCTTATGCTGACACTCACTGACCAACCAAGAGACGA 256
 QY 189 GTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGTACTAAAGATGTTAA 242
 DB 257 GTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGTACTAAAGATGTTAA 310
 RESULT 3
 ID AAV39186 standard; DNA; 490 BP.
 XX AAV39186
 XX

```

AC AAV39186;
DX 01-OCT-1998 (first entry)
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DE Antifungal polypeptide AlfaFP1 encoding cDNA.
XX
KM Antifungal polypeptide; alfalfa plant; Medicago: fungal resistance;
XX plant pathogenic fungus; AlfaFP1; AlfaFP2; ss.
OS Medicago sativa.
XX
FH Key Location/Qualifiers
FT CDS 75..293
FT /tag= a
FT /transl_except= (pos:129..131, aa:Glu)
FT /product= "AlfaFP1 polypeptide"
FT sig_peptide 75..155
FT /tag= b
FT mat_peptide 156..290
FT /tag= c
XX
PN MO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS ) MONSANTO CO.
XX
XX Hakiimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
DR WPI: 1998-348537/30.
DR P-PSDB: AAM61967.
XX
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 5; Fig 1; 97pp: English.
XX
CC This cDNA encodes an antifungal polypeptide, AlfaFP1 isolated from
CC alfalfa plants (Medicago). The polypeptides AlfaFP1 and AlfaFP2 are
CC useful to control plant fungi, especially pathogenic fungi, by
CC transforming plant cells with a vector comprising sequences encoding
CC AlfaFP1 or AlfaFP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 490 BP; 182 A; 85 C; 85 G; 136 T; 2 other:

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Query Match 93.0%; Score 232.4; DB 19; Length 490;
Best Local Similarity 99.6%; Pred. No. 3e-67;
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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0Y 9 CAATCTATCAACATGATGAGAGAAATCAGTGTGCTTCTCTCTTGGT 68
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DB 60 CAATCTATCAACATGATGAGAGAAATCAGTGTGCTTCTCTCTTGGT 119

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OY 69 CTCCTTGTTCACAGAAATGTGTGACAGAGACCAGAAATGTGAGAAATTTGGCAGAT 128
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DB 120 CTCCTTGTTCACAGAAATGTGTGACAGAGACCAGAAATGTGAGAAATTTGGCAGAT 179
OY 129 AATATAGGGGACCATGCTTTAGTGTGTGTGACACTGACGACCAACCAAGAGACCA 188
    |||||||
DB 180 AATATAGGGGACCATGCTTTAGTGTGTGTGACACTGACGACCAACCAAGAGACCA 239
OY 189 GTTACTGGAAGGTGTAGGACGACTTCGCTGCTGTGACTAAAGATGTTAA 242
    |||||||
DB 240 GTTACTGGAAGGTGTAGGACGACTTCGCTGCTGTGACTAAAGATGTTAA 293

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RESULT 4
AAV39190
ID AAV39190 standard; DNA; 200 BP.
XX
AC AAV39190;
XX
DX 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfaFP2 5' region.
XX
KM Antifungal polypeptide; alfalfa plant; Medicago: fungal resistance;
XX plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
XX
OS Medicago sativa.
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
XX Hakiimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
DR WPI: 1998-348537/30.
XX
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 18; Page 75; 97pp: English.
XX
XX This sequence represents the 5' region of the DNA encoding an antifungal
XX polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The
XX polypeptides AlfaFP1 and AlfaFP2 are useful to control plant fungi,
XX especially pathogenic fungi, by transforming plant cells with a vector
XX comprising sequences encoding AlfaFP1 or AlfaFP2 to allow expression of
XX antifungally effective amounts of the polypeptide. Such transformed
XX plants may be e.g. apple, wheat, cotton and especially potato.
XX Micro-organisms may also be transformed to produce the polypeptides, and
XX applied to plants to control plant fungi. The polypeptides can also be
XX included with a suitable solvent in antifungal compositions and these can
XX be administered to plants to control plant fungi. Such compositions and
XX genetically engineered plants may also contain additional molecules e.g.
XX the compositions can contain other antifungal agents or the plants
XX contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
XX proteins. The polypeptides are also useful to prepare antibodies useful
XX to detect polypeptides or isolate other alfalfa plant antifungal protein
XX antigens. The nucleic acids are useful to produce polypeptides and
XX transgenic plants and as probes or primers in nucleic acid hybridisation
XX e.g. to detect complementary sequences in samples, and to prepare mutants
XX or isolate similar sequences from related species.
XX
SQ Sequence 200 BP; 48 A; 36 C; 65 G; 50 T; 1 other:

Query Match 71.9%; Score 179.8; DB 19; Length 200;
Best Local Similarity 98.9%; Pred. No. 6.9e-50;

XX WPI: 1998-348537/30.
 DR Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
 XX - used to control plant pathogenic fungi and to produce transformed
 PT plants with increased fungal resistance
 PS Claim 18: Page 77: 97pp: English.
 XX
 CC This sequence represents the 3' region of the DNA encoding an antifungal
 CC polypeptide. AlfAFP2 isolated from alfalfa plants (Medicago). The
 CC polypeptides AlfAFP1 and AlfAFP2 are useful to control plant fungi,
 CC especially pathogenic fungi, by transforming plant cells with a vector
 CC comprising sequences encoding AlfAFP1 or AlfAFP2 to allow expression of
 CC antifungally effective amounts of the polypeptide. Such transformed
 CC plants may be e.g. apple, wheat, cotton and especially potato.
 CC Micro-organisms may also be transformed to produce the polypeptides, and
 CC applied to plants to control plant fungi. The polypeptides can also be
 CC included with a suitable solvent in antifungal compositions and these can
 CC be administered to plants to control plant fungi. Such compositions and
 CC genetically engineered plants may also contain additional molecules e.g.
 CC the compositions can contain other antifungal agents or the plants
 CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)
 CC proteins. The polypeptides are also useful to prepare antibodies useful
 CC to detect polypeptides or isolate other alfalfa plant antifungal protein
 CC antigens. The nucleic acids are useful to produce polypeptides and
 CC transgenic plants and as probes or primers in nucleic acid hybridisation
 CC e.g. to detect complementary sequences in samples, and to prepare mutants
 CC or isolate similar sequences from related species.
 CC
 XX Sequence 327 BP: 125 A; 49 C; 60 G; 91 T; 2 other;
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 Query Match 47.1%; Score 117.8; DB 19; Length 327;
 Best Local Similarity 94.6%; Pred. No. 3.9e-29;
 Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 114 GAGATTTGGCAGATTAATATAGGGACCATGCTTATGTTGTGACACTCAGTCACA 173
 DB 1 GAGAAATTTGGCGGATAGATATAGGGACCATGCTTATGTTGTGACACTCAGTCACA 60
 QY 174 ACCAAGAGACGACGACTTAGTGGAAGCTGAGGAGACACTTCGGCGTGGCTACTATAA 233
 DB 61 ACCAAGAGACGACGACTTAGTGGAAGCTGAGGAGACTTCGTTGTTAGTGTACTATAA 120
 QY 234 AGATGTTAA 242
 DB 121 AGATGTTAA 129
 RESULT 9
 AAV39196
 ID AAV39196 standard; DNA: 62 BP.
 AC AAV39196;
 XX
 DT 25-SEP-1998 (first entry)
 DE Antifungal polypeptide AlfAFP2 5' gene specific primer.
 XX
 KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
 KM plant pathogenic fungus; AlfAFP1; AlfAFP2; PCR primer; ss.
 XX
 OS Synthetic.
 OS Medicago sativa.
 XX
 PN WO9826083-A1.
 PD 18-JUN-1998.
 PF 11-DEC-1997; 97WO-US22662.
 PR 13-DEC-1996; 96US-0766355.
 XX

PA (MONS) MONSANTO CO.
 XX
 PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
 XX WPI: 1998-348537/30.
 DR
 XX
 PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
 PT - used to control plant pathogenic fungi and to produce transformed
 PT plants with increased fungal resistance
 PS Example 4: Page 78: 97pp: English.
 XX
 CC This primer is used for the PCR amplification of the cDNA encoding an
 CC antifungal polypeptide, AlfAFP2. The antifungal polypeptides AlfAFP1 and
 CC AlfAFP2 isolated from alfalfa plants (Medicago) are useful to control
 CC plant fungi, especially pathogenic fungi, by transforming plant cells
 CC with a vector comprising sequences encoding AlfAFP1 or AlfAFP2 to allow
 CC expression of antifungally effective amounts of the polypeptide. Such
 CC transformed plants may be e.g. apple, wheat, cotton and especially
 CC potato. Micro-organisms may also be transformed to produce the
 CC polypeptides, and applied to plants to control plant fungi. The
 CC polypeptides can also be included with a suitable solvent in antifungal
 CC compositions and these can be administered to plants to control plant
 CC fungi. Such compositions and genetically engineered plants may also
 CC contain additional molecules e.g. the compositions can contain other
 CC antifungal agents or the plants contain DNA encoding insecticidal
 CC (e.g. *Bacillus thuringiensis*) proteins. The polypeptides are also useful
 CC to prepare antibodies useful to detect polypeptides or isolate other
 CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
 CC to produce polypeptides and transgenic plants and as probes or primers in
 CC nucleic acid hybridisation e.g. to detect complementary sequences in
 CC samples, and to prepare mutants or isolate similar sequences from related
 CC species.
 CC
 XX Sequence 62 BP: 18 A; 15 C; 12 G; 17 T; 0 other;
 SQ
 Query Match 24.8%; Score 62; DB 19; Length 62;
 Best Local Similarity 100.0%; Pred. No. 7.6e-11;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGATCCCAATCTATATCAAACTATGAGAGAAATCACTACTGCTTATGCTTCTCT 60
 DB 1 GGGGATCCCAATCTATATCAAACTATGAGAGAAATCACTACTGCTTATGCTTCTCT 60
 QY 61 TC 62
 DB 61 TC 62
 RESULT 10
 AAV39197/c
 ID AAV39197 standard; DNA: 47 BP.
 AC AAV39197;
 XX
 DT 25-SEP-1998 (first entry)
 DE Antifungal polypeptide AlfAFP2 3' gene specific primer.
 XX
 KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
 KM plant pathogenic fungus; AlfAFP1; AlfAFP2; PCR primer; ss.
 XX
 OS Synthetic.
 OS Medicago sativa.
 XX
 PN WO9826083-A1.
 PD 18-JUN-1998.
 PF 11-DEC-1997; 97WO-US22662.
 PR 13-DEC-1996; 96US-0766355.
 XX

PA (MONS) MONSANTO CO.
 XX
 PI Hakim S, Liang J, Rosenberger CA, Shah DM, Wu YS;
 XX WPI: 1998-348537/30.
 DR
 XX
 PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
 PT - used to control plant pathogenic fungi and to produce transformed
 PT plants with increased fungal resistance
 XX
 PS Example 4: Page 78; 97pp; English.
 XX
 CC This primer is used for the PCR amplification of the cDNA encoding an
 CC antifungal polypeptide, AlfAFP2. The antifungal polypeptides AlfAFP1 and
 CC AlfAFP2 isolated from alfalfa plants (Medicago) are useful to control
 CC plant fungi, especially pathogenic fungi, by transforming plant cells
 CC with a vector comprising sequences encoding AlfAFP1 or AlfAFP2 to allow
 CC expression of antifungally effective amounts of the polypeptide. Such
 CC transformed plants may be e.g. apple, wheat, cotton and especially
 CC potato. Micro-organisms may also be transformed to produce the
 CC polypeptides, and applied to plants to control plant fungi. The
 CC polypeptides can also be included with a suitable solvent in antifungal
 CC compositions and these can be administered to plants to control plant
 CC fungi. Such compositions and genetically engineered plants may also
 CC contain additional molecules e.g. the compositions can contain other
 CC antifungal agents or the plants contain DNA encoding insecticidal
 CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
 CC to prepare antibodies useful to detect polypeptides or isolate other
 CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
 CC to produce polypeptides and transgenic plants and as probes or primers in
 CC nucleic acid hybridisation e.g. to detect complementary sequences in
 CC samples, and to prepare mutants or isolate similar sequences from related
 CC species.
 XX
 SO Sequence 47 BP; 11 A; 13 C; 11 G; 12 T; 0 other;
 Query Match 18.8%; Score 47; DB 19; Length 47;
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 204 AGGAGACGACTTCGCTGCTGCTACTAAAGATTAAGATCCCC 250
 DB 47 AGGAGACGACTTCGCTGCTGCTACTAAAGATTAAGATCCCC 1
 RESULT 11
 AA294226
 ID AA294226 standard; DNA: 217 BP.
 XX
 AC AA294226;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Antifungal protein TfeAFP synthetic gene.
 XX
 KW TfeAFP1; antifungal; fungicide; tall fescue; transgenic plant;
 KW crop protection; disease resistance; biological control; PAPFP1; ss.
 XX
 OS Chimeric - Petunia hybrida.
 XX
 OS Chimeric - Festuca arundinacea.
 XX
 PN WO200011178-A2.
 XX
 PD 02-MAR-2000.
 XX
 PF 18-AUG-1999; 99WO-US18866.
 XX
 PR 19-AUG-1998; 98US-0097150.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Liang J, Mitlanck C, Wu Y, Shah D;
 XX

DR WPI: 2000-246567/21.
 XX
 PT Novel nucleic acid encoding Festuca plant antifungal polypeptide 'useful
 PT for producing transgenic plants having resistance to fungal disease
 XX
 XX
 PS Example 4: Page 88; 90pp; English.
 XX
 CC The present sequence is that of a synthetic gene encoding a fusion
 CC between the signal peptide of the petunia antifungal protein PAPFP1
 CC and novel fescue antifungal protein TfeAFP1 mature polypeptide (see
 CC AAY79227). The gene was designed for expression in potato. It was
 CC constructed by PCR amplification (see AA294221-25). TfeAFP1 shows
 CC antifungal activity against Fusarium and Verticillium, and is 1 of
 CC 9 novel antifungal proteins (see AAY79227-35) isolated from fescue
 CC seed. Claimed nucleic acids encoding TfeAFP proteins can be cloned
 CC into vectors for transformation of plant-colonizing microorganisms
 CC or plants, thereby providing a method of inhibiting fungal growth
 CC on plants. The proteins can also be formulated into compositions
 CC useful in controlling undesired fungi.
 XX
 SO Sequence 217 BP; 52 A; 31 C; 53 G; 81 T; 0 other;
 Query Match 16.2%; Score 40.6; DB 21; Length 217;
 Best Local Similarity 60.4%; Pred. No. 0.0017;
 Matches 84; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
 OY 1 GGGATCCCAATCTATATCAAACTATG-GAGAGAATCACTAGCGGCTTATGCTCTC 59
 DB 1 GGGATCCCAATCTATATCAAACTATGAGATATTTCTTCTTATTTTCTTATCTTGGTC 60
 OY 60 TTCTTGCTCTCTTTGTCACAGAAATTTGCTGACAGAGCCAGAACATGTGAGAT 119
 DB 61 TTTTGCTTACTACTCTTCTTACGCTCTATATGTGAGAGTGAAGAGTGTGAGGTGAC 120
 OY 120 TTGCACATTAATATAGG 138
 DB 121 TTTGTCTCTAGATATCG 139
 RESULT 12
 AAQ70126
 ID AAQ70126 standard; cDNA: 141 BP.
 XX
 AC AAQ70126;
 XX
 DT 14-FEB-1995 (first entry)
 XX
 DE Antimicrobial Lc-AFP.
 XX
 KW Antimicrobial; Lc-AFP; symbiosis; disease-resistance;
 KW fungus-resistance; Clavibacter xyli subsp. cynodortlis; CXC;
 KW crop improvement; endophyte; ss.
 XX
 OS Lathyrus cicerca.
 XX
 PN WO9416076-A.
 XX
 PD 21-JUL-1994.
 XX
 PF 05-JAN-1994; 94WO-GB00012.
 XX
 PR 08-JAN-1993; 93GB-0000281.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Dubock AC, Powell KA, Rees SB;
 XX
 WPI: 1994-249223/30.
 DR
 DR P-PSDB: AAR57322.
 XX
 PT Antimicrobial protein producing endo-symbiotic microorganisms -
 PT is produced by combining nucleic acids encoding the protein with
 PT an endophyte, useful for protecting plant hosts from esp. fungal

PT disease
 XX disclosure: Page 30; 39pp.: English.
 XX
 CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC *Citrobacter xyli* subsp. *cynodontis* (Cxc). Plants or seeds treated
 CC with recombinant Cxc are protected against fungal disease. A
 CC suitable antimicrobial protein is Lc-AFP from *L. cicerca*. A
 CC possible predicted sequence for the Lc-AFP gene is given in AAQ70126.
 XX
 SQ Sequence 141 BP: 43 A; 30 C; 32 G; 33 T; 3 other;
 Query Match 16.0%; Score 40; DB 15; Length 141;
 Best Local Similarity 60.6%; Pred. No. 0.0023;
 Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;
 OY 108 ACATGTGAGATTTGGCAGTAATTAAGGAGCATTGCTTACTGCTT-----TGTCAC 161
 DB 4 ACTTGCGAGAACCTTTCTGGAACCTTTCAGAGCCATTCAGATGGAAGTGCAC 63
 OY 162 ACTGACTGACACCAAGAGAGCAGTGTAGTGAAGGTGAGGAGCAGCTTCGCTGC 221
 DB 64 AAGCATTTGCAAGACACAGACATCTTCTTGTGGAAGATGACAGATGATTTCTNNNTGC 123
 OY 222 TGTGTACTAAAGATG 238
 DB 124 TGTGTACTAGAAATCG 140
 RESULT 13
 AAX20260/C
 ID AAX20260 standard; DNA: 9542 BP.
 AC AAX20260;
 XX
 XX 04-MAY-1999 (first entry)
 DE *Borrelia burgdorferi* polynucleotide sequence #13.
 XX
 KW *Borrelia burgdorferi*; spirochete; bacterium; pathogen; Lyme disease;
 KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
 KW infection; diagnosis; characterisation; detection; ds.
 XX
 OS *Borrelia burgdorferi*.
 XX
 PN WO9858943-A1.
 PD 30-DEC-1998.
 XX
 PF 18-JUN-1998; 98WO-US12764.
 XX
 PR 03-SEP-1997; 97US-0057483.
 PR 20-JUN-1997; 97US-0050359.
 PR 22-JUL-1997; 97US-0053344.
 PR 22-JUL-1997; 97US-0053377.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (MEDI-) MEDIMUNE INC.
 XX
 PI Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;
 PI White OR;
 XX
 DR WPI: 1999-081217/07.
 XX
 PT New isolated *Borrelia burgdorferi* nucleic acids - used to develop
 PT products for the detection, diagnosis, characterisation, prevention
 PT and therapy of infections, particularly Lyme disease
 XX
 PS Claim 1; Page 920-925; 1128pp: English.
 XX
 CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from
 CC *Borrelia burgdorferi* (Bb). Products derived from Bb can be used for
 CC the detection, diagnosis, characterisation, prevention and therapy of

CC Bb infections, e.g. Lyme disease. They can also be used for the
 CC production of biosynthetic products, e.g. enzymes. *Borrelia* belongs
 CC to a family of motile, spiral-shaped bacteria called Spirochetes.
 CC Spirochetes are pathogenic in humans and *Borrelia* causes epidemic and
 CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
 CC Lyme disease.
 XX
 SQ Sequence 9542 BP: 3812 A; 1160 C; 1113 G; 3457 T; 0 other;
 Query Match 14.1%; Score 35.2; DB 20; Length 9542;
 Best Local Similarity 52.0%; Pred. No. 0.52;
 Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 OY 23 TATGAGACAGAAATCAGTACGCTGCTTCTCTCTTGGTCTCTTTGTCACA 82
 DB 2597 TATTTAAACAAATTAATATATTGAGTTTACAAAACATAATTTCTTACTGTGAAC 2538
 OY 83 AGAATTTGTGTGACAGAGCCAGACATGTGAGATTTGGCAGATAAATATAGGAGCC 142
 DB 2537 TTAAGTTAAAAAATAATGTAATAAATTACAGTCAAAATTTACAAAATAATATAGGCTAG 2478
 OY 143 ATGCTTAGTGTGTGTGACACTGACACCA 174
 DB 2477 AATAGCTAGTAGTGCTAACATTAATAACAAA 2446
 RESULT 14
 AAQ38648
 ID AAQ38648 standard; DNA: 138 BP.
 AC AAQ38648;
 XX
 XX 07-JUL-1993 (first entry)
 DE Encodes antifungal protein Lc-AFP1.
 XX
 KW *Raphanus sativus*; Brassica; Arabidopsis; Cnicus; *Lathyrus*; *Clitoria*;
 KW fungicide; bactericide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.
 XX
 OS *Lathyrus cicerca*.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..138
 FT /*tag= a
 XX
 PN WO9305153-A.
 PD 18-MAR-1993.
 XX
 PF 27-AUG-1992; 92WO-GB01570.
 XX
 PR 29-AUG-1991; 91GB-0018523.
 PR 13-FEB-1992; 92GB-0003038.
 PR 25-JUN-1992; 92GB-0013526.
 XX
 PA (ICIL) IMPERIAL CHEM IND PLC.
 XX
 PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 XX
 DR WPI: 1993-100978/12.
 XX
 PT Biochemical proteins isolated from seeds of plants - e.g. brassica
 PT or dahlia, useful for increasing plants' resistance to fungal and
 PT bacterial diseases
 XX
 PS disclosure: Fig 31A: 110pp: English.
 XX
 CC This sequence appears to encode antifungal protein Lc-AFP1 from
 CC *Lathyrus cicerca* - see AAR33760. The exact source and isolation of the
 CC sequence is unclear from the specification.
 XX

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 05:14:43 ; Search time 40 Seconds
(without alignments)
1916.730 Million cell updates/sec

Title: US-10-010-731-13
Perfect score: 250
Sequence: 1 GGGGATCCCAATCTAATCA.....AAAGAGCTTAAGATCCCC 250

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PC10S.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	250	3	US-08-766-355-13
2	250	100.0	250	4	US-09-003-198A-13
3	250	100.0	250	4	US-09-428-805-13
4	234	93.6	490	4	US-09-003-198A-19
5	234	93.6	507	4	US-08-766-355-10
6	234	93.6	507	4	US-09-003-198A-10
7	234	93.6	507	4	US-09-428-805-10
8	181.2	72.5	189	4	US-09-003-198A-18
9	179.8	71.9	200	3	US-08-766-355-5
10	179.8	71.9	200	4	US-09-003-198A-5
11	179.8	71.9	200	4	US-09-428-805-5
12	169.6	67.8	293	3	US-08-766-355-6
13	169.6	67.8	293	4	US-09-003-198A-6
14	169.6	67.8	293	4	US-09-428-805-6
15	117.8	47.1	327	3	US-08-766-355-9
16	117.8	47.1	327	4	US-09-003-198A-9
17	117.8	47.1	327	4	US-09-428-805-9
18	62	24.8	62	3	US-08-766-355-11
19	62	24.8	62	4	US-09-003-198A-11
20	62	24.8	62	4	US-09-428-805-11
21	47	18.8	47	3	US-08-766-355-12
22	47	18.8	47	4	US-09-003-198A-12
23	47	18.8	47	4	US-09-428-805-12
24	40	16.0	141	1	US-08-377-687-35
25	40	16.0	141	1	US-08-777-192-35
26	40	16.0	141	4	US-08-971-962-35
27	31.2	12.5	37948	4	US-09-251-645-11

28	30.6	12.2	709	4	US-09-280-116-91	Sequence 91, Appl
29	30.4	12.2	3791	3	US-09-377-310-1	Sequence 1, Appl
30	29.8	11.9	1102	2	US-08-132-990A-1	Sequence 1, Appl
31	29.8	11.9	1102	5	PCT-US92-09382-1	Sequence 1, Appl
32	29.8	11.9	1307	2	US-08-867-030B-6	Sequence 6, Appl
33	29.8	11.9	1307	2	PCT-US95-06119-6	Sequence 6, Appl
34	29.8	11.9	1819	1	US-08-487-753-6	Sequence 6, Appl
35	29.8	11.9	1819	2	US-08-480-065-6	Sequence 6, Appl
36	29.8	11.9	1819	3	US-08-487-744-6	Sequence 6, Appl
37	29.8	11.9	1819	5	PCT-US93-09167-6	Sequence 6, Appl
38	29.8	11.9	2157	2	US-08-132-990A-7	Sequence 6, Appl
39	29.8	11.9	2157	5	PCT-US92-09382-7	Sequence 7, Appl
40	29.8	11.9	2554	2	US-08-627-254C-28	Sequence 28, Appl
41	29.2	11.7	948	3	US-09-135-639-3	Sequence 3, Appl
42	29.2	11.7	1215	2	US-09-092-770-8	Sequence 8, Appl
43	29.2	11.7	1215	4	US-09-222-851-8	Sequence 8, Appl
44	29	11.6	984	4	US-09-134-001C-2705	Sequence 2705, Ap
45	29	11.6	1400	3	US-09-191-099-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-08-766-355-13
: Sequence 13, Application US/08766355
: Patent No. 6121436
: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Maganlal
: APPLICANT: Wu, Yonnie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakim, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: SMREER: P.O. Box 77210
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/766,355
: FILING DATE: Concurrently Herewith
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: MOBT:063
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 250 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-08-766-355-13

Query Match      100.0%: Score 250; DB 3; Length 250;
Best Local Similarity 100.0%: Pred. No. 9.2e-76;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GGGGATCCCAATCTAATCAAGAGAGAAATCACTAGCTGCTTATGCTTCCCT 60
|||||
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Db 1 GGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCTCT 60
QY 1 TCTTGTTCTCTTCTTGTTCACAGAAATTTGTGTACAGAGCCAGAACTATGTGAATTT 120
Db 61 TCTTGTTCTCTTCTTGTTCACAGAAATTTGTGTACAGAGCCAGAACTATGTGAATTT 120
QY 121 TGGCAGATTAATATAGGGAGCCATGCTTTAGTGTGTGACACTCAGCACAACCAAG 180
Db 121 TGGCAGATTAATATAGGGAGCCATGCTTTAGTGTGTGACACTCAGCACAACCAAG 180
QY 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGCTACTAAAGATGTT 240
Db 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGCTACTAAAGATGTT 240
QY 241 AAGATCCCC 250
Db 241 AAGATCCCC 250

RESULT 2

US-09-003-198A-13
: Sequence 13, Application US/09003198A
: Patent No. 6316407

: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Meghmal
: APPLICANT: Wu, Yonnie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakimi, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/003.198A
: FILING DATE: 07-JAN-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT:193
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713) 787-1400
: TELEFAX: (713) 787-1440
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 250 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear

US-09-003-198A-13

Query Match 100.0%; Score 250; DB 4; Length 250;

Best Local Similarity 100.0%; Pred. NO. 9.2e-76; Mismatches 0; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCTCT 60
QY 61 TCTTGTTCTCTTGTTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120
Db 1 TCTTGTTCTCTTGTTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120

Db 61 TCTTGTTCTCTTGTTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120
QY 121 TGGCAGATTAATATAGGGAGCCATGCTTTAGTGTGTGACACTCAGCACAACCAAG 180
Db 121 TGGCAGATTAATATAGGGAGCCATGCTTTAGTGTGTGACACTCAGCACAACCAAG 180
QY 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGCTACTAAAGATGTT 240
Db 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGCTACTAAAGATGTT 240
QY 241 AAGATCCCC 250
Db 241 AAGATCCCC 250

RESULT 3

US-09-428-805-13
: Sequence 13, Application US/09428805
: Patent No. 6329504

: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Meghmal
: APPLICANT: Wu, Yonnie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakimi, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 77210
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/428.805
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/766,355
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: MOBT:063
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 250 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear

US-09-428-805-13

Query Match 100.0%; Score 250; DB 4; Length 250;

Best Local Similarity 100.0%; Pred. NO. 9.2e-76; Mismatches 0; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCTCT 60
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Db 61 TCTTGTTCTCTTGTTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120

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QY	181	AGAACGAGTAGTGGAGGTGTAGGAGCACTTCGCTGCTGTACTAAAGATGTT	240
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QY	241	AAGGATCCCC	250
Db	241	AAGGATCCCC	250


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APPLICANT: Rosenberg, Cindy A.
APPLICANT: Hakim, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 17
OTHER INFORMATION: /mod_base=OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-5

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Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 18 CAGCGTTAAGCTTCTCTCTCTTGGTCTCTTGTTCACAAAGAAATGTGCGACAGAG 77
OY 103 CCAGAACATGTGCAATTTGGCAGATAAATATAGGGACCATGCTTATAGTGTGTGACA 162
Db 78 CCAAGACATGTGCAATTTGGCAGATAAATATAGGGACCATGCTTATAGTGTGTGACA 137
OY 163 CTCACCTGCACACCAAGACAGACGACGTAGTGAAGGTGAGGGACGACTTCCGCTCT 222
Db 138 CTCACCTGCACACCAAGACAGACGACGTAGTGAAGGTGAGGGACGACTTCCGCTCT 197
OY 223 GGT 225
Db 198 GCT 200

RESULT 10
US-09-003-198A-5
Sequence 5, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberg, Cindy A.
APPLICANT: Hakim, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for

```


ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-6

Query Match 67.8%; Score 169.6; DB 3; Length 293;
Best Local Similarity 86.2%; Pred. No. 2.1e-48;
Matches 187; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 129 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTGACGCAACAACAGAGAGAGCA 188
DB 197 ACATACAGGGGACCATGCTTCGTTGTTGTGACTTCACTGCAAAACCAAGACACTTA 256
QY 189 GTTAGTGAAGGTGTAGGAGCAGACTTCCGCTGCTGCT 225
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RESULT 13
US-09-003-198A-6
Sequence 6, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yennie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /mod_base= OTHER
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US-09-003-198A-6

Query Match 67.8%; Score 169.6; DB 4; Length 293;
Best Local Similarity 86.2%; Pred. No. 2.1e-48;
Matches 187; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 9 CAATCTAATCAACATATGAGAGAAATCAGTGGCTTATGCTTCCTCTTGGT 68
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QY 129 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTGACGCAACAACAGAGAGAGCA 188
DB 197 ACATACAGGGGACCATGCTTCGTTGTTGTGACTTCACTGCAAAACCAAGACACTTA 256
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DB 257 CTTAGCGNAGGTGACAGGAGCAGCTTCCGCTGCTGCT 293

RESULT 14
US-09-428-805-6
Sequence 6, Application US/09428805
Patent No. 6329504
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yennie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /note="N = A or C or G or T"
US-09-428-805-6
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Query Match          67.8% Score 169.6; DB 4; Length 293;
Best Local Similarity 86.2% Pred. No. 2.1e-48;
Matches 187; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 9 CAATCTAATCAACATATGAGAGAAATCAGTACGCTTATGCTTCTCTCTCTGTT 68
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DB 197 ACATACAGGGGACATGCTTGTGTGTGTGACTTCACTGCAAAAACAGAGACACTTA 256
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RESULT 15
US-08-766-355-9
Sequence 9, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakim, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one-of(244, 305)
OTHER INFORMATION: /mod_base= OTHER
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US-08-766-355-9
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Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 121 AGATGTTAA 129
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Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 05:33:55 ; Search time 107 Seconds
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3428.568 Million cell updates/sec

Title: US-10-010-731-13

Perfect score: 250
Sequence: 1 GGGGATCCCATCTATCA.....AAAGATGTTAAGATCCCC 250

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
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2	234	93.6	490	US-10-010-731-19	Sequence 19, Appl
3	234	93.6	507	US-10-010-731-10	Sequence 10, Appl
4	181.2	72.5	189	US-10-010-731-18	Sequence 18, Appl
5	179.8	71.9	200	US-10-010-731-5	Sequence 5, Appl
6	169.6	67.8	293	US-10-010-731-6	Sequence 6, Appl
7	119.4	47.8	494	US-09-805-694B-5	Sequence 5, Appl
8	117.8	47.1	327	US-10-010-731-9	Sequence 9, Appl
9	116.4	46.6	563	US-10-178-213-439	Sequence 439, Appl
10	93.4	37.4	420	US-10-178-213-436	Sequence 436, Appl
11	91.6	36.6	464	US-10-178-213-379	Sequence 379, Appl
12	62	24.8	461	US-10-178-213-451	Sequence 451, Appl
13	62	24.8	62	US-10-010-731-11	Sequence 11, Appl
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16	44.2	17.7	438	US-10-178-213-418	Sequence 418, Appl
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22	32.8	13.1	466	9	US-10-178-213-385	Sequence 385, App
23	31.6	12.6	468	9	US-10-178-213-316	Sequence 316, App
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C 41	30.2	12.1	1036	10	US-09-822-849A-415	Sequence 13620, A
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ALIGNMENTS

RESULT 1
US-10-010-731-13
Sequence 13, Application US/10010731
Publication No. US2003004134/7A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-No. US2003004134/7A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBY:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-010-731-13

Query Match 100.0%; Score 250; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.le-74;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-010-731-19
Sequence 19, Application US/10010731
Publication No. US20030041347A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yennie S.

Rosenberger, Cindy A.

Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 490 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-010-731-19

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Best Local Similarity 100.0%; Pred. No. 4.le-69;
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DB 120 CTCCTTGTGACAGAAATGTGTGACAGAACCAAGCAATGTGAANTTTGGCAGAT 128
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RESULT 3

US-10-010-731-10
Sequence 10, Application US/10010731
Publication No. US20030041347A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yennie S.

Rosenberger, Cindy A.

Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

LOCATION: (44)...(271)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (128)...(268)
FEATURE:
NAME/KEY: misc-feature
LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451

Query Match 36.4%; Score 91; DB 9; Length 461;
Best Local Similarity 68.2%; Pred. No. 1.1e-20;
Matches 159; Conservative 0; Mismatches 65; Indels 9; Gaps 2;

QY 19 AACATGAGAGAAATCACTAGCTGGCTTATGCTCTCTTGGTCTTGTG 78
DB 39 AAGCATGGCGGGAAATCTTACCGGTTTGTCTTACCTCCCTCGGTG 98
QY 79 CACAAGAAATTTGGTGACA--GAAGCCAGAACATGTGAGATTGGCAGATAATATA 135
DB 99 CTCAGGAATGTTGGTGAAGTGAAGCAGCAACGTGTAGAACCTGGCGGATACCTACA 158
QY 136 GGGACCATGCTTTA-----GTGTTGTGACACTGCTGCAACCAAGAGAACGAG 189
DB 159 GGGGACCATGCTTACCAACCCGAGACCTGCGAGACCAAGAGAACGAGACCTGC 218
QY 190 TTAGTGAAGGTGTAGGAGCACTCCGCTGCTGTTACTTAAAGATGTAA 242
DB 219 TCAGCGCGCGCTGCGCGACGATTTCCGCTGTTGTGACCAAGAACTGTAA 271

RESULT 13

US-10-010-731-11
Sequence 11, Application US/10010731
Publication No. US20030041347A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yonnie S.

Rosenberger, Cindy A.

Hakim, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 62 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-010-731-11

Query Match 24.8%; Score 62; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGATCCCAATCTAATCAACTATGAGAGAAATCACTAGCTTATGCTTCT 60
DB 1 GGGATCCCAATCTAATCAACTATGAGAGAAATCACTAGCTTATGCTTCT 60
QY 61 TC 62
DB 61 TC 62

RESULT 14

US-10-178-213-427

Sequence 427, Application US/10178213

Publication No. US20030041348A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Navarro Acevedo, Pedro A.

APPLICANT: Harvell, Leslie

APPLICANT: Cahoon, Rebecca

APPLICANT: McCutchen, Billy Fred

APPLICANT: Lu, Albert

APPLICANT: Hermann, Rafael

APPLICANT: Mong, James

TITLE OF INVENTION: Defensin Polynucleotides and Methods of

FILE REFERENCE: 35718/246703

CURRENT APPLICATION NUMBER: US/10/178,213

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: 60/300,152

PRIOR FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: 60/300,241

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 427

LENGTH: 338

TYPE: DNA

ORGANISM: Cyamopsis tetragonoloba

FEATURE:

NAME/KEY: CDS

LOCATION: (14)...(244)

NAME/KEY: mat.peptide

LOCATION: (101)...(241)

US-10-178-213-427

Query Match 19.5%; Score 48.8; DB 9; Length 338;

Best Local Similarity 52.5%; Pred. No. 2e-06;

Matches 107; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 24 ATGAGAGAAATCACTAGCTGCTTATGCTTCTTGTGCTTGTGCTTGTG 83

DB 20 ATGATGAGAAATCACTAGCTTGTGCTTCTTCTTCTTCTTCTTCTTCT 79

QY 84 GAAATTTGCTGACAGAGCCAGAACATGTGAGAAATTTGGCAGATAATATA 143

DB 80 ATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 139

QY 144 TCGTTAGTGCTTGTGAGACCTGCTGACCAACCAAGAGAGAGAGAGAG 203

DB 140 TCGTTGAGAGACCAATACCTGCTGCTGAGAGAGAGAGAGAGAGAGAG 199

QY 204 AGGAGACCTCCGCTGCTGTGT 227

DB 204 AGGAGACCTCCGCTGCTGTGT 227

Db 200 TGCCGAGGTTTCGCCGTGCTGT 223

RESULT 15

US-10-010-731-12/C

; Sequence 12, Application US/10010731

; Publication No. US20030041347A1

; GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Hu, Yonnie S. Cindy A.

Rosenberger, Cindy A.

Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-010-731-12

Query Match 18.8% Score 47; DB 9; Length 47;

Best Local Similarity 100.0%; Pred. No. 2.9e-06;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

204 AGGAGCACTTCGCTGCTGCTGCTAAAGATGTAAGATCCCC 250

|||||

47 AGGAGCACTTCGCTGCTGCTGCTAAAGATGTAAGATCCCC 1

|||||

Search completed: June 21, 2003, 06:17:16

Job time : 109 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 03:56:28 ; Search time 1132 Seconds
(Without alignments)
3576.742 Million cell updates/sec

Title: US-10-010-731-13
Perfect score: 250
Sequence: 1 GGGGATCCCAATCTAATCA.....AAAAGATGTTAGAGATCCC 250

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estdb:*
2: em_esthm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184.6	73.8	446	9	AJ498901 AJ498901
2	118.2	47.3	574	14	B0151477 B0151477
3	118	47.2	517	9	AJ308155 AJ308155
4	116.2	46.5	487	13	BI321179 BI321179
5	114.6	45.8	426	12	BG838678 BG838678
6	102.8	41.1	503	12	BF633403 BF633403

7	87.6	35.0	438	13	BI642738
8	61.4	24.6	238	13	BI642792
9	49	19.6	366	9	AJ503961
10	49	19.6	366	13	BI321308
11	49	19.6	447	13	BI269947
12	49	19.6	450	12	BG450155
13	49	19.6	452	12	BG452703
14	49	19.6	466	14	B0157500
15	47	18.8	543	12	BG453394
16	43.8	17.5	372	9	AJ498451
17	42.8	17.1	319	9	AJ375191
18	42	16.8	550	9	AL373581
19	41.8	16.7	203	9	AL379949
20	41.8	16.7	354	9	AL376623
21	41.8	16.7	383	9	AL379948
22	41.8	16.7	432	9	AL377785
23	41.8	16.7	436	9	AL378977
24	41.8	16.7	440	9	AL380895
25	41.8	16.7	443	9	AL375904
26	41.8	16.7	445	9	AL375903
27	41.8	16.7	450	9	AL377784
28	41.8	16.7	456	9	AL377705
29	41.8	16.7	459	9	AL377706
30	41.8	16.7	461	9	AL380896
31	41.8	16.7	473	9	AL373658
32	41.8	16.7	479	9	AL375897
33	41.8	16.7	483	9	AL380879
34	41.8	16.7	490	9	AL376002
35	41.8	16.7	491	9	AL374748
36	41.8	16.7	534	10	AW980646
37	41.8	16.7	552	9	AL374749
38	41.8	16.7	701	14	B0255321
39	40.2	16.1	418	9	AL377999
40	40.2	16.1	494	9	AL373580
41	39.4	15.8	331	12	BG453276
42	39.4	15.8	475	13	BI269021
43	38.6	15.4	364	9	AJ498976
44	38.6	15.4	452	12	BG451938
45	38	15.2	454	12	BG451992

ALIGNMENTS

RESULT 1
AJ498901
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
barrel medic.
Medicago truncatula
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Rosidae: eurosids I: Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 446)
Firnhaber,C., Bartelsmeier,V., Meyer,F., Bartels,D., Bekel,T.,
Linke,B., Puehler,A. and Kuester,H.
Determination of transcript sequences from developing pods
including seeds of Medicago truncatula genotype Al7
Unpublished (2002)
JOURNAL
COMMENT
Contact: Kuester H
Lehrstuhl fuer Genetik
Universitaet Bielefeld
Postfach 100131, D-33501 Bielefeld, Germany.
Location/Qualifiers
1..446
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="mt-acc955209h10"

BASE COUNT	147 a	84 c	83 g	132 t
ORIGIN				
Query Match	73.8%	Score 184.6	DB 9	Length 446:
Best Local Similarity	87.4%	Pred No. 2.7e-47		
Matches	202	Conservative	0	Mismatches 29; Indels 0; Gaps 0;
Oy	12	TCTAATCAACTATGAGAGAGAAATCTACTAGCTGGCTTATGCTTCCTCTTGGTTC	71	
Db	49	TATCACTAAGCTATGAGAGAGAAACATACAGACGCTATGCTTCCTCTGCTCTC	108	
Oy	72	TTTGTGGACAGAAATTTGGTGTACACAGAACCCAGACATGTGAGAAATTTGGCAGATAA	131	
Db	109	TTTGTGGACAGAAATTTGGTGTACACAGAACCTAAGACTTGTGAGAAATTTGGCAGATAA	168	
Oy	132	TATAGGGACCATGCTTTAGTGTGTGTGACACTCACTCAACACCAAGAGAACCGACTT	191	
Db	169	TACAGGGACCATGCTTTAGTGTGTGTGATCACTCACTCACTACCAAGAGAAATGCACTT	228	
Oy	192	AGTGAAGGTGTAGGAGACACTTCCGCTGCTGGTGTACTAAAGATGTAA	242	
Db	229	AGCGGACGTCAGAGGATGACTTTCGTTGGTGTACTAAAACTGTAA	279	
RESULT 2				
LOCUS	B0151477	574 bp	mRNA	linear
DEFINITION	NF088A06LF1038 Developing leaf Medicago truncatula cDNA clone			
ACCESSION	B0151477			
VERSION	B0151477.1 GI:20288536			
KEYWORDS	EST.			
SOURCE	barrel medic.			
ORGANISM	Medicago truncatula			
REFERENCE	Medicago truncatula			
AUTHORS	Eunatryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.			
TITLE	1 (bases 1 to 574)			
JOURNAL	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.			
COMMENT	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library			
	Unpublished (2000)			
	Contact: May GD			
	Plant Biology Division			
	The Samuel Roberts Noble Foundation			
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA			
	Tel: 580 221 7391			
	Fax: 580 221 7380			
	Email: gdmay@noble.org			
	Insert Length: 574 Std Error: 0.00			
	Plate: 088 row: A column: 06			
	Seq primer: TCACACAGAAACAGCATATGAC.			
FEATURES				
Source	Location/Qualifiers			
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	/db_xref="taxon:3880"			
	/clone="NF088A06LF"			
	/clone_lib="developing leaf"			
	/tissue_type="leaf"			
	/dev_stage="pooled developmental"			

[illegible][illegible]

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 Db 127 TTGTTGCACAGAAATTTGGTGACAGAACCCAGACATGTGAGATTTGGCAGATTAAT 186
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 QY 133 ATAGGGACCATGCTT-----TAGTGGTTGTACACTCAGTCCACACCAAGACAGC 186
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 Db 187 TCAGGAGCATTGATCCAGATGCTGACCAACAACTTCAGAGAACAGACGACT 246
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 QY 187 CAGTTAGTGAGAGTGGAGGAGGAGTCCGCTGCTGTGTACTAAAGATGTTAA 242
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 Db 247 TACTAGTGGAGAGTCCAGGAGATTTTGGCTGCTGTGTACTCCAAACTGTTAA 302
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RESULT 4
 B1321179
 LOCUS
 DEFINITION B1321179 487 bp mRNA linear EST 29-NOV-2001
 saf8d10.y3 Gm-cl077 Glycine max cDNA CLONE GENOME SYSTEMS CLONE
 ID: Gm-cl077-1723 5, similar to SW:10KD_VIGUN_P18646.10 KD PROTEIN
 PRECURSOR ;, mRNA sequence.
 B1321179
 ACCESSION B1321179.1 GI:15000365
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 487)
 Shoemaker, R., Keim, P., Vodka, L., Erpelting, J., Corvett, V., Rhanna
 A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schunk
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Putative full length read
 vector to vector length is This clone is available through: Resgen,
 Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801
 For further information call: (800)-533-4363 or contact via email:
 ccl@resgen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 432.
 Location/Qualifiers
 1.487
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl077-1723"
 /clone_1ib="Gm-cl077"
 /tissue_type="18 day old 'Williams' seedlings"
 /dev_stage="18 day old 'Williams' seedlings"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+; Site: 1: EcoRI; Site: 2:
 XhoI; The mRNA was isolated from cotyledons of 18-day-old
 'Williams' seedlings which were greenhouse grown in
 potting soil. The cotyledons were flash-frozen in liquid
 nitrogen. Stratagene's cDNA Synthesis Kit (catalog number
 200401) was used to synthesize the cDNA. First-strand
 synthesis was performed with 5-methyl dCTP, hence the
 ligated cDNA was hemimethylated. A modification of
 Stratagene's first-strand synthesis primer was used. An
 'anchor' nucleotide (Y=A, C, or G) was added to the 3' end
 of the primer (GAGAGAGAGAGAGAGAGACTGCTCGAG(T)18V) to
 anchor the primer at the 5' end of the poly(A) tract.
 After second-strand synthesis, the cDNA ends were filled

BASE COUNT 152 a 96 c 102 g 137 t
 ORIGIN
 Query Match 46.5%; Score 116.2; DB 13; Length 487;
 Best Local Similarity 74.1%; Pred. NO. 1e-25;
 Matches 177; Conservative 0; Mismatches 53; Indels 9; Gaps 2;
 QY 13 CTATCAACTATGAGAGAAATCACTAGCTGCTATGCTTCCTCTTGGTCTCT 72
 |||||
 Db 57 CTATATTAAGCATGAGAGAAATCACTAGCTGCTTCCTCTTCTTCTCTCT 116
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 QY 73 TTGTTGCACAGAAATTTGGTG---ACAGAACCCAGACATGTGAGATTTGGCAGATA 129
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 Db 117 TTGTTGCACAGAAATTTGGTGCAAACTGAGCAAAAGCTTGAGAACCTGCGCATATA 176
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 QY 130 AATATGGGAGCATGCTT-----TAGTGGTTGTACACTCAGTCCACACCAAGACAGA 183
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 Db 177 CATACAGGGGCTCATGCTTACCACTGCGAGCTGCGATGTTCTGCAAGAACAAAGAGC 236
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 QY 184 ACCGAGTTAGTGAGAGGTGAGGAGAGCTCCGCTGCTGTACTAAAGATGTTAA 242
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 Db 237 ACTTGCTCAGAGCAGATGAGGAGGAGCATTTTGGCTGCTGTGTCACCAAAACTGTTAA 295
 |||||

RESULT 5
 BG838678/c
 LOCUS
 DEFINITION BG838678 426 bp mRNA linear EST 25-MAY-2001
 Gc01_03f01_A Gc01_AAFc_ECORC_cold_stressed_Glycine-clandestina
 Glycine clandestina cDNA clone Gc01_03f01, mRNA sequence.
 BG838678
 VERSION BG838678.1 GI:14204985
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Glycine clandestina.
 Glycine clandestina
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 426)
 Singh, J.A., Farah, S., Chapados, J., Couroux, P., De Moors, A., Harris
 L., J., Hattori, J., Ouellet, T., Robert, L., S., Spott, D. and Tinker
 N.A.
 Expressed Sequence Tags from Cold-Stressed Glycine clandestina
 Seedlings
 Unpublished (2001)
 Contact: Singh, J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-Food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
 0C6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@agr.ca
 Location/Qualifiers
 1.426
 /organism="Glycine clandestina"

In with cloned Pfu DNA, ligated to EcoRI adapters and
 subsequently phosphorylated. The cDNA was then
 precipitated and redissolved in sterile, RNase-
 Dnase-free water. The XhoI site within the first- strand
 synthesis primer was then restricted by digestion with
 XhoI from Promega (400U/ul); all XhoI sites in the cDNA
 would be protected by their hemimethylated status. The
 cDNA constructs were size-fractionated with a 500bp
 cutoff, using Sephacryl S-500 High Resolution (Pharmacia
 Biotech) in a 2-mm diameter column and a bed volume of
 approximately 1ml. The column eluent was precipitated,
 redissolved, and ligated into Stratagene's pBluescript II
 XR Predigested vector (pBluescript II SK(+)) vector that
 has been digested with EcoRI and XhoI, and phosphorylated
 by Stratagene). This library was constructed in the
 Laboratory of Dr. Paul Keim and Dr. Virginia H. Corvett at
 Northern Arizona University."

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/cultivar="1035"
/db_xref="taxon:45687"
/clone="Gc01_03f01"
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1na"
/tissue_type="Leaves, stem"
/note="Vector: Bluescript SK+/XhoI-ECORI; site_1: ECORI;
site_2: XhoI; Plants incubated at 2 degrees under 12 hours
of light/day. Harvested after only 2-3 days of cold
treatment. cDNA was prepared with the uni-zap cDNA kit
from Stratagene. Eco RI adapters were ligated followed
by digest with Xho I/Eco RI and ligated to pBluescript."
116 a 92 c 86 g 125 t 7 others

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Query Match	45.8%;	Score 114.6;	DB 12;	Length 426;
Best Local Similarity	70.7%;	Pred. No. 3.2e-25;		
Matches 176;	Conservative	6;	Mismatches 58;	Indels 9;

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 Db 416 ATATCACTGAGCCATGAGAGAATACTACTTGCATGATTTGCTTCTCTTCCTGCTCT 357

Oy	7	CTTGTGGCAAGAATTGCGTG---	ACAGAGCCGAACATGTGAATAATTGCAGA	127
Db	356	CTTTGTGCACAAGAA TTGTGGTGAANA	CTGAGCCAAACACTTCGCGA GAACCTGGCTAA	2977

Qy	128	TAATAATAGGGAGCCATGCTTTA-----GTGGTTTGACACACTCATGACACAAACCAAGA	181
Db	296	TACATATACAGGGGTCATGCTTACCTACCGGACAGCTGCGATGATCATCTGCACAGATATAAGA	237

Qy 182 GAAGCAGTTAGTGCAGAGGTGTAGGGACGACTTCCCTGCTGCTGTGTTCTAAAGATCTTA 241
Db 236 ACACCTACTCAGCGCAGGTGCAGGCAVATTTTCGCTGHTGGHGCACCAGAACTGTTA 177

QY	242	AGGATCCCC	250
		: :	
Db	176	ATTAGMCS	168

RESULT	6
BFF633403	
LOCUS	BFF633403
DEFINITION	BFF633403
	NF047E803D1F1022 Drought Medicago truncatula cDNA clone NF047E03DT 5', mRNA sequence.
	503 bp linear EST 19-DEC-2000

VERSION	Bf6333403.1	GI:11897561
KEYWORDS	EST.	
SOURCE	barrel medic.	
ORGANISM	Medicago truncatula	

REFERENCE
1 (bases 1 to 503)

AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, C.J., Flores, H. R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
JOURNAL Unpublished (2000)

COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
tel: 580 221 7391

Fax: 580 221-7380
Email: gdmay@noble.org
Insert Length: 503 Std Error: 0.0
Plate: 047 row: E column: 03
Seq primer: TCACACAGGAACAGCTATGAC.

```
FEATURES      Location/Qualifiers
source        1..503
              /organism="Medicago truncatula"
```

Query Match	41.1%	Score 102.8	DB 12	Length 503
Best Local Similarity	72.7%	Pred. No. 1.8e-21		
Matches 176; Conservative	0	Mismatches 37	Indels 9	Gaps 3

QY 5 CAACTAATCAAACTATGGAGAAATAACTACTGGC TTATGCTTCTCTTCTGGT 67
Db 4 9 CACTATCATTTAAGCATGGAGAAATAATCAATACCTGGCGTGTGCTTACTCTTCTCTG 108

Oy 68 TCCTCTTTGTCACAGAAATTGGGTGACAGAAGCCAGAACATGTGAGAAATTGGCAGA 127
| | | | | | | | | | | | | | | | | | | | | |
Db 109 TCTCTTTGTCACAGAAATTGGGGACTGACAGAAGCACTTGTGAGCAATTTGGCTGA 168

Qy 128 TAAATATAGGGGACCATGCTTTA-----GTGTTGTGACTCAGTGCACAACCAAGA 181
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 169 TACATTACAGAGGACCATTGCTTCACGGAAGTAGTGATGACCACTGCAGACACAAAGC 228

OY 182 GAACGCGATTAGTGAAGGTGTAGS6A CCACTCCGCCTGCTGGTGTAATAAGATGTTA 241
 ||| |||| | | | | | | | | |
Db 229 ACACITAAATTAGTSCA--CCGTCATTACTTTCATGTTTCTGCACACAAAACGTGTTA 286

Qy	242	Ag	243	.	.	.
Db	287	Ag	288			

RESULT 7
BI642738

Sumner) *Robinia pseudoacacia* cDNA, mRNA sequence.
 accession
 version
 keywords
 source
 GI:15544948
 BI642738
 EST.
Robinia pseudoacacia.

Eukaryota; Viridiplan-
Spermatophyta; Magnoli-
Rosidae; eurosids I;
Robinia.

REFERENCE	1 (Pages 1 to 436)
AUTHORS	Han, R.-H., Yang, J., Park, S., Paule, C. R., Kapur, V., Retzel, E. F., Kende, D. P. and Keathley, D. E.
TITLE	Analysis of gene expression patterns in trunk wood of a mature black locust (<i>Robinia pseudoacacia</i>)

JOURNAL COMMENT
Unpublished (2002)
Contact: Kyung-Hwan Han
Department of Forestry
Michigan State University
16 Natural Resources, East Lansing, MI 48824-1222, USA

FEATURES
source 1. .438
 Email: hanky@msu.edu,
 Location/Qualifiers
 Tel: 517 353 4751
 Fax: 517 432 1143

```

/organism="Robinia pseudoacacia"
/db_xref="taxon:35938"
/clone_id="TZ5 (Sapwood-heartwood transition zone of
black locust - Summer)"
/tissue_type="sapwood-heartwood transition zone"

```

```

/dev_stage="mature tree"
/Note="Vector: lambda Triplex; Site_1: Sfi IA; Site_2: Sfi
IB; The cDNA library was made from the sapwood-heartwood

```


OY 15 AATCAACTATGAGAAATACACTAGCTGCTTATGCTTCTCTTCTGTTCTTT 74
 Db 11 AAGAGAGTATGAGAGAAACACTGCTAGCTGTGCTTCTTCTCATTTGTTCTCTTA 70
 OY 75 GTTGACACAGAAATTTGTGCTG 95
 Db 71 GCTGCTCAAGACAGCATGTGCTG 91

RESULT 12
 BG450155
 LOCUS
 DEFINITION
 NC014H03DTP11032 Drought Medicago truncatula cDNA clone NF014H03DT
 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 barrel medic.
 Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Location/Qualifiers
 1. 450
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF014H03DT"
 /clone_lib="Drought"
 /tissue_type="Plantlets"
 /dev_stage="Pooled timepoints"
 /note="Vector: Lambda Zap; Contains a mixture of entire
 plantlets harvested in a series of days-post-watering
 timepoints."
 158 a 60 c 89 g 143 t

BASE COUNT
 ORIGIN
 Query Match 19.6% Score 49; DB 12; Length 450;
 Best Local Similarity 75.3%; Pred. No. 0.00016;
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

FEATURES
 source
 1. 450
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF014H03DT"
 /clone_lib="Drought"
 /tissue_type="Plantlets"
 /dev_stage="Pooled timepoints"
 /note="Vector: Lambda Zap; Contains a mixture of entire
 plantlets harvested in a series of days-post-watering
 timepoints."
 158 a 60 c 89 g 143 t

BASE COUNT
 ORIGIN
 Query Match 19.6% Score 49; DB 12; Length 450;
 Best Local Similarity 75.3%; Pred. No. 0.00016;
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 15 AATCAACTATGAGAAATACACTAGCTGCTTATGCTTCTCTTCTGTTCTTT 74
 Db 12 AAGAGAGTATGAGAGAAACACTGCTAGCTGTGCTTCTTCTCATTTGTTCTCTTA 71
 OY 75 GTTGACACAGAAATTTGTGCTG 95
 Db 72 GCTGCTCAAGACAGCATGTGCTG 92

RESULT 13
 BG452703
 LOCUS
 DEFINITION
 NC079E01LF 5', mRNA sequence.
 452 bp mRNA linear EST 16-MAR-2001
 Medicago truncatula cDNA clone
 ACCESSION
 VERSION
 BG452703.1 GI:13371497

KEYWORDS
 SOURCE
 ORGANISM
 EST.
 barrel medic.
 Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Location/Qualifiers
 1. 452
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF079E01LF"
 /clone_lib="Developing leaf"
 /tissue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Contains a mixture of very
 young, developing, mature and senescing leaves."
 158 a 60 c 89 g 145 t

BASE COUNT
 ORIGIN
 Query Match 19.6% Score 49; DB 12; Length 452;
 Best Local Similarity 75.3%; Pred. No. 0.00016;
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

FEATURES
 source
 1. 452
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF079E01LF"
 /clone_lib="Developing leaf"
 /tissue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Contains a mixture of very
 young, developing, mature and senescing leaves."
 158 a 60 c 89 g 145 t

BASE COUNT
 ORIGIN
 Query Match 19.6% Score 49; DB 12; Length 452;
 Best Local Similarity 75.3%; Pred. No. 0.00016;
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

FEATURES
 source
 1. 452
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF079E01LF"
 /clone_lib="Developing leaf"
 /tissue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Contains a mixture of very
 young, developing, mature and senescing leaves."
 158 a 60 c 89 g 145 t

BASE COUNT
 ORIGIN
 Query Match 19.6% Score 49; DB 12; Length 452;
 Best Local Similarity 75.3%; Pred. No. 0.00016;
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

RESULT 14
 B0157500
 LOCUS
 DEFINITION
 NC105E08IR1F1067 Irradiated Medicago truncatula cDNA clone
 B0157500
 466 bp mRNA linear EST 24-APR-2002
 Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

